

94199

**From:** Hamud, Fozia  
**Sent:** Friday, May 16, 2003 9:48 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** sequence search for 09/912,157

RECEIVED

MAY 16 2003

Please search 09/912,157, SEQ ID NO:2 amino acid residues 36-313, 36-753, 336-753 and 1-753 against commercial data bases and interference data bases. Thank you.

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 Patent Examiner  
 Art Unit 1647  
 Crystal-Mall-One, Room 10Bo5  
 Mail Box CM1-10B19  
 308-8891

Point of Contact:  
 Toby Port  
 Technical Info. Specialist  
 CM1 6A04  
 703-308-3534

Searcher: \_\_\_\_\_  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: 5/19  
 Date Completed: 5/19  
 Searcher Prep/Review: \_\_\_\_\_  
 Clerical: \_\_\_\_\_  
 Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
 AA Sequences: 4  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
 DRLink: \_\_\_\_\_  
 Lexis/Nexis: \_\_\_\_\_  
 Sequence Sys.: cg  
 WWW/Internet: \_\_\_\_\_  
 Other (specify): \_\_\_\_\_

GenCore version 5.1.4.p5.4578  
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On protein: protein search, using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 15.4315 seconds  
(without alignments)  
2804.041 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_336\_753

Perfect score: 2210

Sequence: 1 RKQENIYSHLDESESS.....QADLCRSYTDLHVAAPL 418

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_73:\*

1: piri:\*

2: piri:\*

3: piri:\*

4: piri:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2210	100.0	564	2	T42695
2	150.5	6.8	846	2	T27282
3	126	5.7	718	2	T30113
4	110	5.0	535	2	T17212
5	107.5	4.9	3942	2	T42730
6	105.5	4.8	592	2	T49239
7	105	4.8	757	2	T09081
8	105	4.8	901	2	JC6093
9	105	4.8	1571	2	T14155
10	100.5	4.5	901	2	F83781
11	99.5	4.5	734	2	S59069
12	98	4.4	1023	2	T48937
13	97.5	4.4	291	2	F86451
14	97.5	4.4	589	2	F96599
15	96.5	4.4	438	2	T38930
16	96.5	4.4	981	1	F0MVGW
17	96	4.3	660	2	S31437
18	95	4.3	933	1	ORHUP
19	95	4.3	2148	2	A56011
20	94	4.3	469	2	T46929
21	94	4.3	429	2	T46930
22	93.5	4.2	471	2	B85170
23	93.5	4.2	806	1	JN0612
24	93.5	4.2	807	1	I51153
25	93.5	4.2	1571	2	T00062
26	93	4.2	499	2	T34328
27	93	4.2	1557	2	T13160
28	92.5	4.2	531	2	T08760
29	92.5	4.2	546	2	JC4798

30	92.5	4.2	2314	1	A45151
31	92	4.2	883	2	S57653
32	92	4.2	985	2	A96777
33	92	4.2	3147	2	T21328
34	91.5	4.1	348	2	T34266
35	91	4.1	883	2	S49126
36	91	4.1	2038	2	A43742
37	90.5	4.1	828	2	T33481
38	90.5	4.1	3788	2	T13960
39	90	4.1	579	2	JT0494
40	90	4.1	627	2	T27123
41	89.5	4.0	641	2	T05497
42	89.5	4.0	766	2	S37894
43	89.5	4.0	3507	2	T34513
44	89	4.0	357	2	T03785
45	89	4.0	1337	2	T13948

ALIGNMENTS

RESULT 1

T42695

hypothetical protein: DKFZp434N128.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

C:Accession: T42695

R:Bioecker, H.; Boecker, M.; Brandt, P.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: T22230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFZp434N128

C:Genetics:

A:Note: DKFZp434N128.1

Query Match 100.0% Score 2210; DB 2; Length 564;

Best Local Similarity 100.0%; Pred. No. 3.6e-170;

Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RKQENIYSHLDESESSYTTAALPRRLPRPKVFLCYSSKDGQNHNNVQCFAYFL	60
DB	147	RKQENIYSHLDESESSYTTAALPRRLPRPKVFLCYSSKDGQNHNNVQCFAYFL	206
QY	61	QDFCCCEVALDLWEDSLCRQREWVTKIHESQFIIVCSKGMKVFVKNNKHEGG	120
DB	207	QDFCCCEVALDLWEDSLCRQREWVTKIHESQFIIVCSKGMKVFVKNNKHEGG	266
QY	121	RGSKGELFLVANSATAEKLQAKOSSAALSKFIAYFDYSCSDVPGLDLSTYRLM	180
DB	267	RGSKGELFLVANSATAEKLQAKOSSAALSKFIAYFDYSCSDVPGLDLSTYRLM	326
QY	181	DNLPQLCSHLSDHGLQEPQRTQGRSRRYFRSKSGSLVAICNNHOFIDEEPWF	240
DB	327	DNLPQLCSHLSDHGLQEPQRTQGRSRRYFRSKSGSLVAICNNHOFIDEEPWF	386
QY	241	KQVFPFPPPLRYRPEVLEKFPGLVANDVCKPGSPDFCLKVEAAVLGATGPDQS	300
DB	387	KQVFPFPPPLRYRPEVLEKFPGLVANDVCKPGSPDFCLKVEAAVLGATGPDQS	446
QY	301	SGHGLDGDGARPALDGSAAQLPLHTVTKAGSPDMPDSDGYDSSVPSSELSL	360
DB	447	SGHGLDGDGARPALDGSAAQLPLHTVTKAGSPDMPDSDGYDSSVPSSELSL	506
QY	361	LSTDQETSSITSSVSSSGSGGEGEPALPSKLLSSGCKADLCGRSTYTDLHVA	418
DB	507	LSTDQETSSITSSVSSSGSGGEGEPALPSKLLSSGCKADLCGRSTYTDLHVA	564

RESULT 2

T27282  
 hypothetical protein Y64G10A.e - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C:Accession: T27282  
 R:Almough, R.  
 submitted to the EMBL Data Library, September 1999  
 A:Reference number: Z20336  
 A:Accession: T27282  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-846 <NLS>  
 A:Cross-references: EMBL:AL110498; PIDN: CAB54470.1; CESP: Y64G10A.e  
 A:Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e

Query Match 6.8%; Score 150.5; DB 2; Length 846;  
 Best Local Similarity 22.5%; Pred. No. 0.00065;  
 Matches 94; Conservative 57; Mismatches 147; Indels 119; Gaps 24;

QY 2 KKOQNTYSHLDESSSESYTALPRESLRPRKPVLYCYSSKQGNHNVVQCFAYFLQ 61  
 DB 448 KKKASNI--ELLNPAFSS--HSGSIFL--ILKQISVLVLY--SHDSQAHEAVTAFELLR 502  
 QY 62 DFCQCEVALDWEFSCRCQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 121  
 DB 503 DVFMLNVLHDVWDEDDI--EENRAEYINSSIVRANKVIIINSIG--AYF--RTVFRQR-- 555  
 QY 122 GSGKGLFLVAVSAITAELKQAKSSAALSFKTAVFYDSCGDV--PGILDLSYK-- 177  
 DB 556 -----EPAIERITITGRND-----VIFDMQCELALQHPVCSHFSTYN 593  
 QY 178 -----RLMD--NLPLQSLHSHDGLQEPQHTQSGRRNYPSSGSRSLYVAICN 227  
 DB 594 PKVFFPNNLLQYSIP--NSLMTWTALTQPARPEQLAGNQVFAR-----LQALSR 646  
 QY 228 MHQFIDEEPDETEK-----QVPPHPHPLYR-----EP 256  
 DB 647 KLVIESDQWENTHNRVATRVSELAHNIVPL--PFSLEVYEDVAFQOMTILDE 705  
 QY 257 VLEKF-----DSGLVINDVCKPGPSDPCLVKVAANVIGATGPADSOHESQH 303  
 DB 706 LKFNPAKNDLEVEVLSQVLEKDKVCAQGP-----IHVEFTEFVLEPAEPMEAE 760  
 QY 304 GGLDQDGEARPALDGSAA-----LQPLL--HTVKGSPDMRSDSGIYDSS--VPSSELS 354  
 DB 761 ED-EEDEDDVDVSGQTARIEELQLIVH-----KDMNHDGSLDSATVSGSDFS 809

RESULT 3  
 T30113

hypothetical protein F56D1.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T30113  
 R:Chlasoe, S.; Wilson, R.  
 submitted to the EMBL Data Library, November 1995  
 A:Description: The sequence of C. elegans cosmid F56D1.  
 A:Reference number: Z20737  
 A:Accession: T30113  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-718 <CHI>  
 A:Cross-references: EMBL:U39997; PIDN: AAA81100.1; CESP: F56D1.2

C:Gene: CESP:F56D1.2  
 A:Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2

Query Match 5.7%; Score 126; DB 2; Length 718;

Best Local Similarity 21.1%; Pred. No. 0.049;  
 Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;  
 QY 28 REIRLRPR-----KYFLCYSSKQGNHNVVQCFAYFLQDQCEVALDWEFDS 77  
 DB 398 RDKVRSREVRNTATFVKVNIYAD--DNLDFTCVKVLNLRNCASCDVPFLEKLT 456  
 QY 78 LCREGQREVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRSGKGEFLFVAVSA 137  
 DB 457 AEQIVPSRLVDTSSLKKEIIVVSCAEKILDTSETHQLVOARPPADLEGFAMEI- 515  
 QY 138 EKLQAKQSSAALSFKTAVFYDSCGDV---GILDSTKYRLMDMLPCLCSHLHSD 194  
 DB 516 --IRDTHNFPPEARKKAVVRNTS--PHVPPNLAAILNLT--FILPEQFAQLTAFLHVE 570  
 QY 195 HGLOEPQHTQSGRRNYPSSGSRSLX---VAICNMQHOFIDEEPDETEKQFVP- 245  
 DB 571 H-----TERANVTQNISEAQIHEWNLCLASRMSSFFVYRNPNWLETWRKDELAA 619  
 QY 246 FHPPLRYREPVLEKFPDGLVINDVCKPGPSDPCLVKVAANVIGATGPADSOHESQHG 305  
 DB 620 LH--LRQSPVYPIQI-----EED---RIASIKYLNLYVPPQALVDS- 657  
 QY 306 LQDGEARPALDGSAAQLPPLLHTVKGSPDM--PRDSGIYDSSVPSSELSLPLMEGLST 363  
 DB 658 -DED-----DVDLQ--HASHONQPLILPPEQCG-----PDS-SD 690  
 QY 364 DOTETSSLTSSVSSSGLGEPEPPALPSK 392  
 DB 691 SEDSSSESSESQNEG---EDPKTIVK 716

## RESULT 4

T17212  
 hypothetical protein DKFZP434P211.1 - human (fragments)

C:Species: Homo sapiens (man)  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T17212  
 R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18723  
 A:Accession: T17212  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-488; 489-535 <POD>  
 A:Cross-references: EMBL:AL117401  
 A:Experimental source: adult testis; clone DKFZP434P211  
 A:Note: the cDNA sequence contains a -1 frameshift near codon 488  
 C:Genetics:  
 A:Note: DKFZP434P211.1

Query Match 5.0%; Score 110; DB 2; Length 535;

Best Local Similarity 23.5%; Pred. No. 0.65;  
 Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 139 KLEQAQSS--SAALSKEIATVYDSCGDVPGI-----LDLSTKYRLMDNLPO 185  
 DB 103 RYNOTSOTSWTSCTNNALSSYSSTGGLGLRRRGPASSHCOLTSSSTVSDRQ 162  
 QY 186 LASHLHSDHGLQ--PGQHTQSGRRNYPSSGSRSLYVAICNMQHOFIDEEPDETEKQF 243  
 DB 163 AVSSGHTQCEKAADIAPQTLT--LRNDSSTSEASRP-----STHKF---PLLPRRG 210  
 QY 244 VPH-PPPL-----RYREPVLKFPDGLVINDV---CKPGPSDPCLVKVA 287  
 DB 211 EPLMPPPLEGLVYVYEDLDREKAAPQINSALQVEDKALSDCRSPSH---TLSSL 267  
 QY 288 VLGANG--PADSOHESQHGGLDQGEARPALDGSAAQLPPLLHTVKGSPDM- 340  
 DB 268 ATGAGLFAVSKAPS-----MDAQQETHKSDCLGLDPLASA--AGVPTAPMSGKKRRP 321  
 QY 341 SG-IYDSSVPSSELSPLMEGLSTQDTSTSLTESVSSSGSLGEEPPALPSKLLSSG 397  
 DB 341 SG-IYDSSVPSSELSPLMEGLSTQDTSTSLTESVSSSGSLGEEPPALPSKLLSSG 397

I49239 vesicle transport protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I49239  
 R:Tellam, J.F.; McIntosh, S.; James, D.E.  
 J. Biol. Chem. 270, 5857-5863, 1995  
 A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neurone  
 A:Reference number: I49238; MUID:95197608; PMID:7890715  
 A:Accession: I49239  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-592 <RES>  
 A:Cross-references: EMBL:U19521; NID:9642027; PIDN:AAA69913.1; PID:g642028  
 C:Genetics:

Best Local Similarity    20.6%;    Pred. No. 2.6;  
Matches                 92;      Conservative    42; Mismatches    147; Indels    166; Gaps    23;

	QY	11	HLDSESESITTAALP-----RERLRPRKVF-----LCYSRRSGDNMMVVO	54     : ::      ::  : :      :
	Dd	169	HYRVDTQTWGTATLPDIPEDAFISHKLTKPLIVRESTNLSVLVSRTAEHMSGWT	228     :
	QY	55	CF-AIFYLDFCGCEVALDMDESLFCRGQEHWIOKHESOFIIVCSGMKIYFDVK--	111   : : :     :   : : :     :
	Dd	229	CYDAVRVVVD--ECRAETDIW-----NGQRD-----RIIVTCT'S-KELVARLA	267   : : :     :   : : :     :
	QY	112	----KNYHKGGGRGS-----KGSELFLVAVSIAEKLURQAOKSSSAALSXFIA	156   : : :     :   : : :     :





A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA804773.1; GSPDB:GN00  
A:Experimental source: strain C:125  
A:Gene: BH1034

Query Match: 4.5%; Score 100.5; DB 2; Length 901;  
Best Local Similarity: 22.6%; Pred. No. 7.6;  
Matches 66; Conservative 44; Mismatches 103; Indels 79; Gaps 15;

QY 1 RKQOENIYSHLDE-----ESSESTYATAPRELPRPVPFVCISSDKQGN 48  
DB 482 RKTDSVPGVQKMLGRHLRKGESVHLELGLVAL-AHMLRKRATV--DRRSKEPKN 538

QY 49 ---RM---VVOCF---AVFIADFCGEVALDLWEDFSICREGREW--- 87  
DB 539 TQHKHRENIKRSRYVLCRWDSPPFIISDQKQYASPALED--KLRRGGENMIEVI 596

QY 88 -IOKIHESOFIIVCSKGMKVFYDKNKYKHGGSGKGELFLVAVSAI- 136  
DB 597 DLKSTINRQVY---KGMVFTEKGMVGLPGAGKASTTSMISSLIQPTSGDVLK 652

QY 137 ---AEKLRQSSAALSKEFTAVFYDSC-----GDVPGILDSTKYRLMDNLPQLC 187  
DB 653 GGSIHQSKAIRSILGVVPOEIAVYHDITARENLAFFGIYGLKGEELKHE--NESTLQLV 711

QY 188 SHLSRDRGLQPGHTRQGRNFRSKGRSLYVAICNMHQ---FIDREP 236  
DB 712 ---GLEE---RQNDVHTFSGMKRRNLNIAVALLHEPELLIMDEP 750

Query Match: 4.5%; Score 99.5; DB 2; Length 794;  
Best Local Similarity: 20.6%; Pred. No. 7.7; Indels 87; Gaps 15;

QY 64 CGCEVALDWEFSLCHREGQREWIQIHESOFIIVCSKGMK-VFYDKNKYKHGGSG 122  
DB 24 CDCFTFYD-GVDF-----KAHKA-VLAACSEYFMFLFYDQKDVHLDISNA 67

QY 123 SGKGEFLVAVSAIAELKROAKOSS-----AALSKEFTAVFYDSCGDVPGILDST 175  
DB 68 AGLGQ-----VLEFMYTAKLSLSPENVDDVLAVASPLQMG-----DIVT 106

QY 176 KYRLMDNLPQLCSHL-HSRDGLQEPQGE-----TRQGRNFRSKGRSLY 222  
DB 107 ACTHIAASPSSTGSDASASAVEGDKRAKDEKAAATHLSRLQAGSSSTGGRELK 166

QY 223 VATCNMQHPIDEPMTKEQVFPFPPPLRYREPVLKFTDGLVLDVCMKPGPESDFCL 282  
DB 167 EERGQAESAGSAGABOTEKADAPREPP-----VELKPDPTSSMA- 206

QY 283 KVEAYVLGATGPASQESQGRGLDQGEARPDGSAALQPLHTVYKAGSPSPDRSG 342  
DB 207 AAEEAALSSSEBOEVEPASKG--EDQGEAGAGATVKEGMEH-LONGEPPEENESA 263

QY 343 IYDSSVPSSELSLP---LMELSTDTQTTSSITSSVSSSSGLGEE 384

DB 264 GTDS---GOELGHEGQNLRSYTGRTESRAYSGSIHRCDCGKE 305  
RESULT 12  
T48997

epsin-like protein - Arabidopsis thaliana  
N:Alternate names: protein P25L23.150  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000

R:Accession: T48997  
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.  
submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25012  
A:Accession: T48997  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-1023 <DAN>  
A:Cross-references: EMBL:AL356014; GSPDB:GN00061; ANSP:P25L23.150

C:Genetics:  
A:Gene: ATSP:P25L23.150  
A:Map position: 3  
A:Introns: 12/2; 29/3; 56/2; 82/3; 110/3; 159/2; 263/2; 277/2; 311/2; 365/3; 443/3; 8

Query Match: 4.4%; Score 98; DB 2; Length 1023;  
Best Local Similarity: 20.4%; Pred. No. 14;  
Matches 76; Conservative 55; Mismatches 146; Indels 96; Gaps 17;

QY 85 ENVIQIHESOFIIVCSKGMKVFYDKNKYKHGGSGKGELFLVAVSAIAELKROAK 144  
DB 96 ERVIEVEHEHAYQITLS-GFYQ-IDSSG---KDGSNVYKKAQSLVALYNDKERITEVR 150

QY 145 QSSSALSKEP-----IAVYD-YSCGDVPGILDSTKYRLMDNLPQLCSHLRSDHG 196  
DB 151 EKAAANDKYNHMRPSGGYDKYDYG-----RYGRDGRSSYKEREIG 198

QY 197 LQEPQCHTRQGRNFRSKGRSLYVAICNMHQFIDEPDMFEKQFVFPFPPPLRYREP 256  
DB 199 YRDDRNRSDGR--YSRDSEDR--YGRDGN---TDDE-----YGRSR 235

QY 257 VLEKFDGLVLDVCMKPGPESDFCLKVE---AAVLGATGPADSQESQGRGLDQ--- 309  
DB 236 SYDNYG-----SRGSSDRERPIEDDQSSRDGADDDHSGDGRGLERKFE 286

QY 310 ---GEARPDGSAALQPLHTVYKAGSPDRSGIYDSSVPSSELSLPLMEGLSTDTQ 366  
DB 287 QNIGAAPSYEAVS-----ESRSPYSERDGGTQVAPPAGAAASPLAENISVDNK 338

QY 367 EYSSLTE-----SYSS-SSGLSEEPALPSKILLS-----GSKADLGC 405  
DB 339 AADFNESSPQVAFEDFDPKGSVSACATAGASVAFIPPTVTVSTPAPPASINAEML 398

QY 406 RSYTDELHVAPL 418  
DB 399 LAGSLSDVFSNPFL 411

RESULT 13  
F86451

protein F6N18.2 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: F86451  
C:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Li, J.H.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzbeg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25012  
A:Accession: T48997  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-1023 <DAN>  
A:Cross-references: EMBL:AL356014; GSPDB:GN00061; ANSP:P25L23.150

C:Genetics:  
A:Gene: ATSP:P25L23.150  
A:Map position: 3  
A:Introns: 12/2; 29/3; 56/2; 82/3; 110/3; 159/2; 263/2; 277/2; 311/2; 365/3; 443/3; 8

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PID:11130712  
 A:Accession: F86451  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-291 <STO>  
 A:Cross-references: GB:AE005172; NID:g6714285; PIDN:AAF79311.1; GSPDB:GN00141  
 A:Genetics: F8618.2  
 A:Map position: 1

Query Match 4.43; Score 97.5; DB 2; Length 291;  
 Best Local Similarity 24.28; Pred. No. 2.9;  
 Matches 47; Conservative 28; Mismatches 76; Indels 43; Gaps 10;  
 QY 229 HOIDEIPWFEKQVPPHPPPLRYREPVL---EFDSGLVNDVCKRGPDSFCLKVE 285  
 DB 92 HEFVARP-----PHEPLP-HGQPIIISGDFGSGNTAESV-----SVTKYR 133  
 286 AAVLGATGADSGHESQGGGLDQ---DGEAR-----PALDGSAAOLPLHRTVAGSPSD 336  
 134 QSLGSGPNEOMQPSHDNQQQPVESQAQSHNHGSPFNDSARNTPILTPKFDGPPQ 193  
 QY 337-NPRDSGLTSDVSPSSLSLPLMGLSTDDTETSSLTESVSSSGLGEPEPALSKLSS 396  
 DB 194 Q-----HNNSLPS-----PFRNGILPTTSQYRP--QSPRYNNLLSPRSPLIST 241  
 QY 397 G-SCKADLCGRSYT 409  
 DB 242-GVQTPPLTPRNT 255

## RESULT 14

F96599  
 protein F1A1J16.6 [Imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 A:Accession: F96599  
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, F.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PID:11130712  
 A:Accession: F96599  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-589 <STO>  
 A:Cross-references: GB:AE005173; NID:g8778302; PIDN:AAF79311.1; GSPDB:GN00141  
 A:Genetics: F1A1J16.6  
 A:Map position: 1

Query Match 4.43; Score 97.5; DB 2; Length 589;  
 Best Local Similarity 20.09; Pred. No. 7.5;  
 Matches 60; Conservative 34; Mismatches 123; Indels 63; Gaps 12;  
 QY 104 GMFYVDKNTKHKGGGSGKGELEFVAVSAIAEKLRQAKQSSAALSFKTAVTFDYSC 163  
 DB 88 GRNFASSNSYQSSGRNASKRE---NGANHVTRGSRTAQPATKASNITVPNETKVS 144  
 QY 164 EGDVPGILDLSKYRLMDNLPOL--CSHLSRDHGLQEPGQHTROGSRNRYFRSKGRSL 221  
 DB 145 PASIPSEV---SNHQAQD--PLISASRCSSKSDQATEIETASKQKNSL----- 191  
 QY 222 TVACNHEQFIDEEDPWFQFV---PFHPPLRYRPEVLEKFSGLVNDVCKRGPDS 279  
 DB 192 -----PKPDVSEQSHVTFPFH-----LQVAKGLQGLTFGSP-----DSN 226

QY 280 FCLKYRAAVLGATGADSGHESQGGGLDQGEARPALDGSAAALQPL-----LFTVKA 331  
 DB 227 FVEKYSVS-NGASGGYDSNFESSHGTGDDERESSPTNGITGVASARFVTEILSLYLRE 285  
 QY 332 GSPDMPDRSDIYDSS-----VPSSELSIPLMEGLSTDDTETSSLTESVSSSGLGEPE 386  
 DB 286 TSTVSEDKDIGLSGATGAEFVHSDHIVPPVEVPFKEALSNETHQIA-----YQEAR 341  
 RESULT 15  
 I38946  
 melanoma ubiquitous mutated protein - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 31-May-1996 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
 A:Accession: I38945; I38946  
 R:Coulle, P.G.; Lehmann, F.; Lethe, B.; Herman, J.; Lurquin, C.; Andrawiss, M.; Boon,  
 Proc. Natl. Acad. Sci. U.S.A. 92, 7976-7980, 1995  
 A:Title: A mutated intron sequence codes for an antigenic peptide recognized by cytotoxic  
 A:Reference number: I38944; MUID:95372402; PMID:7644523  
 A:Accession: I38945  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-438 <RES>  
 A:Cross-references: EMBL:U70897; NID:g1046222; PIDN:AAC50240.1; PID:g1046223  
 A:Accession: I38946  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'G', 1-74 <RES>  
 A:Cross-references: EMBL:U70908; NID:g1046218; PIDN:AAC50238.1; PID:g1046219  
 C:Genetics:  
 A:Introns: 46/73

Query Match 4.43; Score 96.5; DB 2; Length 438;  
 Best Local Similarity 20.84; Pred. No. 6.1;  
 Matches 94; Conservative 39; Mismatches 135; Indels 183; Gaps 24;  
 QY 65 GCVALDMEQDFILCRGQEWIKHESQFIIVCCKGMYFVKKKYNKKGGRGSG 124  
 DB 30 GCK-----YVLCRWKRLNPAKVLART- - - - -TSTNKRRK----- 61  
 QY 125 KGELEVA-----VSAIAEKLRQAKQSSAALSFK-----TA 156  
 DB 62 --EYFVQVILSLEKIKVSTVEILEKSOEIAIASSLASONVPAAPLEELAYRSLR 119  
 QY 157 VYFDYSCEDV-----PGILDLSKYRLMDNLPOLC-----SHLGR 193  
 DB 120 VALDVLSEGSINWSSAGTGRADSLRQKPMHVSPPCDNSSSLPRGDLVLSRRPHRR 179  
 QY 194 -----DH--GLQEP-----GQHTROGSR---RNT- 212  
 DB 180 RVCVQSLSSSTCEKDPCKDCKVKKRKSXENRPGPLVLPAGGAQDESGRIEHNWT 239  
 QY 213 FRKSGR--SLYVAICNNHOFI---DEPDNFEK---QFVFPHPPLRYRPEV---LEKPD 262  
 DB 240 LASKRGRNSAKASICLNGSSISEDDTERDMGSGGSAWAPSLPSCVREDPCANAGHD 299  
 QY 263 SGVLVNDVCKRGPDSFCLKVEAVVAGATGADSGHESQGGGLDQGEARPALDGS--- 319  
 DB 300 PGLPLGLSLTAPPAPPSAC-----SEPG--ECPAKRPRLDGSGRP 338  
 QY 320 --AALQPLHRTVAGSPDMPDRSDIYDSSVPSSELSI-PLMEGLSTDDT----- 366  
 DB 339 PAVOLEPM---AAGAASPSPG--GPGPESVTPRSTARLGGPPPSHASADATCLPCPDQSK 394  
 QY 367 ---ETSSLTESVSSSGLG-----EPEPP 387  
 DB 395 LEKESSEESGMSNRSILEDEDEDEPP 425

Search completed: May 19, 2003, 09:25:32  
 Job time : 22.4315 secs



Pt growth, and modulating immune system by binding to endogenous zcytor18 ligand

Claim 1; Page 2; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 amino acid sequence.

XX  
SQ Sequence 753 AA;

Query Match 100.0%; Score 4013; DB 23; Length 753;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAPVLQCSVFFTVNACLSQAVAGSGRGADTCGRKFAAARPLCVANEGVGP	60
DB	1	MAPVLQCSVFFTVNACLSQAVAGSGRGADTCGRKFAAARPLCVANEGVGP	60
QY	61	ASRSGLYNITFKYDNCITLYNPGKEVYADQAQNTISQYACHDQAVATILSPGALGIE	120
DB	61	ASRSGLYNITFKYDNCITLYNPGKEVYADQAQNTISQYACHDQAVATILSPGALGIE	120
QY	121	FLGFRVILBELSGRQCQQLILKDPKQNSFKRTGNSQPLNKKFETDFYFKVVPF	180
DB	121	FLGFRVILBELSGRQCQQLILKDPKQNSFKRTGNSQPLNKKFETDFYFKVVPF	180
QY	181	PSIKNESNYHPPFRACDILLQPNLACKPFWPRNLISQSGSDQVSDHAPNFG	240
DB	181	PSIKNESNYHPPFRACDILLQPNLACKPFWPRNLISQSGSDQVSDHAPNFG	240
QY	241	FRFTLYHLKHEGFKKTKCQQTETTSCLQNSPGDYIELVDQNTTRKVMHYA	300
DB	241	FRFTLYHLKHEGFKKTKCQQTETTSCLQNSPGDYIELVDQNTTRKVMHYA	300
QY	301	LAPVHSPWAGPIRAVAITVPLVVISAPATLFTVMCKKQENIYSHLDESESTYTA	360
DB	301	LAPVHSPWAGPIRAVAITVPLVVISAPATLFTVMCKKQENIYSHLDESESTYTA	360
QY	361	LPRLRPRKPVLCYSSKQGNEMVYVOCFAFLQDFCGCEVALDLWEDFSLCREGORE	420
DB	361	LPRLRPRKPVLCYSSKQGNEMVYVOCFAFLQDFCGCEVALDLWEDFSLCREGORE	420
QY	421	WVIOKIHESQILVWCCKGNYFDKNNKKGSGSGKGLFLVAVSNIAKLRQAKO	480
DB	421	WVIOKIHESQILVWCCKGNYFDKNNKKGSGSGKGLFLVAVSNIAKLRQAKO	480
QY	481	SSAALSKEFNTFYCEGDPVGLDSTKFLMDNTPQLCSHLSDRHGLQEPQTR	540
DB	481	SSAALSKEFNTFYCEGDPVGLDSTKFLMDNTPQLCSHLSDRHGLQEPQTR	540
QY	541	QGSRRNTFRSKGRSLIYAICNMHQFIDEEDPWFKEQVPPPPPLRYREPYLEKFD	600
DB	541	QGSRRNTFRSKGRSLIYAICNMHQFIDEEDPWFKEQVPPPPPLRYREPYLEKFD	600
QY	601	VLVDMCKPQSPDCLKVAZVAVLGATGPADSOHESQHGGLDQGEARPALDGSAAQPL	660
DB	601	VLVDMCKPQSPDCLKVAZVAVLGATGPADSOHESQHGGLDQGEARPALDGSAAQPL	660
QY	661	LVTVKAGSPDMRPGSLYVDSVSSLSPLMEGLSTDTQETSSLTSESVSSSGLGEE	720
DB	661	LVTVKAGSPDMRPGSLYVDSVSSLSPLMEGLSTDTQETSSLTSESVSSSGLGEE	720

QY 721 PPALPSKLLSSGSCRADLGCRSTTDELAVAPL 753  
DB 721 PPALPSKLLSSGSCRADLGCRSTTDELAVAPL 753

RESULT 2

ABB07627  
ID ABB07627 standard; Protein; 753 AA.

AC ABB07627;

DT 20-MAY-2002 (first entry)

XX Human cytokine receptor, zcytor18 variant sequence.

XX Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;  
KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 369 /label= r269W

FT /note= 'wild-type Thr is replaced with Met'

FT Misc-difference 750

FT /label= V750A

FT /note= 'wild-type Val is replaced with Ala'

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23253.

XX 26-JUL-2000; 2000US-220747P.

XX (ZWO ) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX N-PSDB; ABA95033, ABA95034.

XX New cytokine receptor polypeptide designated zcytor18, useful for

XX inhibiting cell proliferation associated with psoriasis or tumor

XX growth, and modulating immune system by binding to endogenous zcytor18

XX ligand

XX Disclosure; Page 94-98; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 variant amino acid sequence.

XX Sequence 753 AA;

Query Match 99.8%; Score 4003; DB 23; Length 753;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPWLOLCSVEFTVNAVLINGSLAVAGSGRGADTCGRWKAARPRCLVANEGVGP 60  
 Db 1 MAPWLOLCSVEFTVNAVLINGSLAVAGSGRGADTCGRWKAARPRCLVANEGVGP 60  
 QY 61 ASRNSGLYNTFFKIDNCTTYLNPVGRVIAADQNTTISQYACHDQVAVTILSPGALGIE 120  
 Db 61 ASRNSGLYNTFFKIDNCTTYLNPVGRVIAADQNTTISQYACHDQVAVTILSPGALGIE 120  
 QY 121 FLKGFVRLIELKSEGRCCOOLILKDPKQLNSFFKRTGKESOPFLNKKFETDYFKVVPF 180  
 Db 121 FLKGFVRLIELKSEGRCCOOLILKDPKQLNSFFKRTGKESOPFLNKKFETDYFKVVPF 180  
 QY 181 PSIKNESNYHPFFFRACDLLOPNLACKPFWKPRNLNTSQHSDMOVSFDHAPHNFG 240  
 Db 181 PSIKNESNYHPFFFRACDLLOPNLACKPFWKPRNLNTSQHSDMOVSFDHAPHNFG 240  
 QY 241 FRFFLYHLKHEGPKRTCKQBOTTTETSCLLQNVSPGDIYIELVDDTNTTRKVMYA 300  
 Db 241 FRFFLYHLKHEGPKRTCKQBOTTTETSCLLQNVSPGDIYIELVDDTNTTRKVMYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVISAFAITLVYVCKKQOENIYSHLDEESSESTYAA 360  
 Db 301 LKPVHSPWAGPIRAVAITVPLVISAFAITLVYVCKKQOENIYSHLDEESSESTYAA 360  
 QY 361 LPRERLAPRPRKVFCLYSSKDGQNNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 Db 361 LPRERLAPRPRKVFCLYSSKDGQNNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 QY 421 WYIOKIHESQFIIVVCSKGMKYFYDKNTYKHKGGSGKGLFLVAVSAIAELKRAQK 480  
 Db 421 WYIOKIHESQFIIVVCSKGMKYFYDKNTYKHKGGSGKGLFLVAVSAIAELKRAQK 480  
 QY 481 SSSAALSKFTAVTFDYSCGDPVGLDLSKYELMDNLPOLCSHLHSDRGLOEPQOTR 540  
 Db 481 SSSAALSKFTAVTFDYSCGDPVGLDLSKYELMDNLPOLCSHLHSDRGLOEPQOTR 540  
 QY 541 QSSRNTFRSKGRSLYVAICNMHQFIDEEPWFKEQVFPHPPLRYEPVLEKFDGSL 600  
 Db 541 QSSRNTFRSKGRSLYVAICNMHQFIDEEPWFKEQVFPHPPLRYEPVLEKFDGSL 600  
 QY 601 VLDNVCNKPESDFCLRYEAALVILGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 660  
 Db 601 VLDNVCNKPESDFCLRYEAALVILGATGPADSOHESQHGGLDQGEARPALDGSAAQLPL 660  
 QY 661 LETVYKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGLGEE 720  
 Db 661 LETVYKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGLGEE 720  
 QY 721 PPALPSKLLSGGSKRADLCGRSYTDELHAAVPL 753  
 Db 721 PPALPSKLLSGGSKRADLCGRSYTDELHAAVPL 753

RESULT 3  
 ABB07628  
 ID ABB07628 standard; Protein; 739 AA.  
 XX AC ABB07628;  
 XX DT 20-MAY-2002 (first entry)  
 XX DE Human cytokine receptor, Zcytor18 splice variant.  
 XX KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;  
 XX KW Pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 XX KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.  
 XX OS Homo sapiens.  
 XX PN WO200208259-A2.  
 XX PD 31-JAN-2002.  
 XX

PF 23-JUL-2001; 2001WO-US23253.  
 XX 26-JUL-2000; 2000US-220747P.  
 XX (2YMO) ZYMOGENETICS INC.  
 PA Presnell SR, Kuestner RE, Gao Z;  
 PI WPI; 2002-217048/27.  
 DR N-PSDB; ABA95035; ABA95036.  
 XX  
 PT New cytokine receptor polypeptide designated zcytor18, useful for  
 PT inhibiting cell proliferation associated with psoriasis or tumor  
 PT growth, and modulating immune system by binding to endogenous zcytor18  
 PT ligand  
 XX  
 XX Claim 1: Page 102-106; 119pp; English.  
 CC The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumor growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 splice variant.  
 XX  
 XX Sequence. 739 AA.

Query Match 97.8%; Score 3925; DB 23; Length 739;  
 Best Local Similarity 98.1%; Pred. No. 0;  
 Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 1 MAPWLOLCSVEFTVNAVLINGSLAVAGSGRGADTCGRWKAARPRCLVANEGVGP 60  
 Db 1 MAPWLOLCSVEFTVNAVLINGSLAVAGSGRGADTCGRWKAARPRCLVANEGVGP 60  
 QY 61 ASRNSGLYNTFFKIDNCTTYLNPVGRVIAADQNTTISQYACHDQVAVTILSPGALGIE 120  
 Db 61 ASRNSGLYNTFFKIDNCTTYLNPVGRVIAADQNTTISQYACHDQVAVTILSPGALGIE 120  
 QY 121 FLKGFVRLIELKSEGRCCOOLILKDPKQLNSFFKRTGKESOPFLNKKFETDYFKVVPF 180  
 Db 121 FLKGFVRLIELKSEGRCCOOLILKDPKQLNSFFKRTGKESOPFLNKKFETDYFKVVPF 180  
 QY 181 PSIKNESNYHPFFFRACDLLOPNLACKPFWKPRNLNTSQHSDMOVSFDHAPHNFG 240  
 Db 181 PSIKNESNYHPFFFRACDLLOPNLACKPFWKPRNLNTSQHSDMOVSFDHAPHNFG 240  
 QY 241 FRFFLYHLKHEGPKRTCKQBOTTTETSCLLQNVSPGDIYIELVDDTNTTRKVMYA 300  
 Db 241 FRFFLYHLKHEGPKRTCKQBOTTTETSCLLQNVSPGDIYIELVDDTNTTRKVMYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVISAFAITLVYVCKKQOENIYSHLDEESSESTYAA 360  
 Db 301 LKPVHSPWAGPIRAVAITVPLVISAFAITLVYVCKKQOENIYSHLDEESSESTYAA 360  
 QY 361 LPRERLAPRPRKVFCLYSSKDGQNNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 Db 361 LPRERLAPRPRKVFCLYSSKDGQNNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 QY 421 WYIOKIHESQFIIVVCSKGMKYFYDKNTYKHKGGSGKGLFLVAVSAIAELKRAQK 480  
 Db 421 WYIOKIHESQFIIVVCSKGMKYFYDKNTYKHKGGSGKGLFLVAVSAIAELKRAQK 480  
 QY 481 SSSAALSKFTAVTFDYSCGDPVGLDLSKYELMDNLPOLCSHLHSDRGLOEPQOTR 540  
 Db 481 SSSAALSKFTAVTFDYSCGDPVGLDLSKYELMDNLPOLCSHLHSDRGLOEPQOTR 540

Db 467 SSSAALSKFIAVFDYSCGVDVPGILDLSTKYRLMDNIPQLCHLSRDRHGLQEPQHTR 526  
 QY 541 QGSRNTRFKSGRLXVAICNMQHFDIDEPWFQKQVFFHPPLRYPVLEKFSGL 600  
 Db 527 QGSRNTRFKSGRLXVAICNMQHFDIDEPWFQKQVFFHPPLRYPVLEKFSGL 586  
 QY 601 VLNDVCKPGPESDFCLVAEAVLGATGPADSOHSGRGGGLDQGEARPDGSAALQPL 660  
 Db 587 VLNDVCKPGPESDFCLVAEAVLGATGPADSOHSGRGGGLDQGEARPDGSAALQPL 646  
 QY 661 LFTVAGSPDMPRDGIYDSSVPSSELSPLMECLSTDDTSTSSLTSSSSGLGEE 720  
 Db 647 LFTVAGSPDMPRDGIYDSSVPSSELSPLMECLSTDDTSTSSLTSSSSGLGEE 706  
 QY 721 PPALPKILLSGSCRADIGCKNSTYDELHVAPL 753  
 Db 707 PPALPKILLSGSCRADIGCKNSTYDELHVAPL 739

## RESULT 4

AAU09904  
 ID AAU09904 standard; Protein; 738 AA.

AC AAU09904;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein.

KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; cachexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human.

OS Homo sapiens.

PN W0200168859-A2.

PD 20-SEP-2001.

PF 15-MAR-2001; 2001WO-US08678.

PR 16-MAR-2000; 2000US-189816P.

PR 28-NOV-2000; 2000US-0724460.

PA (AMGR-) ANGEN INC.

PI Jang S;

PT WPI; 2001-611392/70.

DR N-PSDB; AAS15346.

PT Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 diabetes, psoriasis and glaucoma.

PS Claim 2; Page 152-154; 158pp; English.

CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal

CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, melanoma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17R may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17R antibodies and antagonists may also be used to down regulate  
 CC expression and activity. This is the amino acid sequence of the human  
 CC Interleukin 17 (IL-17) receptor like protein described in the method of  
 CC the invention.

XX Sequence 738 AA;

Query Match 97.2%; Score 3901; DB 22; Length 738;  
 Best Local Similarity 97.6%; Pred. No. 0;

Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPYQLCSVFTTNAACLSQLAAVAGSGRAGADTCGRKAAARPRCLVANGVGP 60

Db 1 MAPYQLCSVFTTNAACLSQLAAVAGSGRAGVDTGMR-----GVGP 46

QY 61 ASRNSGLYNITFKYDNCNTTYLAPVGRKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 120

Db 47 ASRNSGLYNITFKYDNCNTTYLAPVGRKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 106

QY 121 FLGFRVILELSEKSGRQCQQLILDKPKLNSFKRTGMSOPFLNMFFETDYVKKVVP 180

Db 107 FLGFRVILELSEKSGRQCQQLILDKPKLNSFKRTGMSOPFLNMFFETDYVKKVVP 166

QY 181 PSIKNESNYHPPFTRACDLILDPNLACPPKPKPNLNISQHSQDMQVDFHAPRNG 240

Db 167 PSIKNESNYHPPFTRACDLILDPNLACPPKPKPNLNISQHSQDMQVDFHAPRNG 226

QY 241 FREFTLRLKLEHGPFRKTKQEQTTTSCILLONVSPDYIIIEVDNTTKVNHYA 300

Db 227 FREFTLRLKLEHGPFRKTKQEQTTTSCILLONVSPDYIIIEVDNTTKVNHYA 286

QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQENIYSHLDESSSSTYTA 360

Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQENIYSHLDESSSSTYTA 346

QY 361 LPRERLRPRKPVFLCTSSKDGQNMNVQCFAYFLQDFCGCEVALDLWEDFSLCRGORE 420

Db 347 LPRERLRPRKPVFLCTSSKDGQNMNVQCFAYFLQDFCGCEVALDLWEDFSLCRGORE 406

QY 421 WYQKHESQFIIVVCSKGMKYVDKNNYHKGSGSGKSGELFLVAVSAIEKLQAKQ 480

Db 407 WYQKHESQFIIVVCSKGMKYVDKNNYHKGSGSGKSGELFLVAVSAIEKLQAKQ 466

QY 481 SSSAALSKFIAVFDYSCGVDVPGILDLSTKYRLMDNIPQLCHLSRDRHGLQEPQHTR 540

Db 467 SSSAALSKFIAVFDYSCGVDVPGILDLSTKYRLMDNIPQLCHLSRDRHGLQEPQHTR 526

QY 541 QGSRNTRFKSGRLXVAICNMQHFDIDEPWFQKQVFFHPPLRYPVLEKFSGL 600

Db 527 QGSRNTRFKSGRLXVAICNMQHFDIDEPWFQKQVFFHPPLRYPVLEKFSGL 586

QY 601 VLNDVCKPGPESDFCLVAEAVLGATGPADSOHSGRGGGLDQGEARPDGSAALQPL 660

Db 587 VLNDVCKPGPESDFCLVAEAVLGATGPADSOHSGRGGGLDQGEARPDGSAALQPL 646

QY 661 LFTVAGSPDMPRDGIYDSSVPSSELSPLMECLSTDDTSTSSLTSSSSGLGEE 720

Db 647 LFTVAGSPDMPRDGIYDSSVPSSELSPLMECLSTDDTSTSSLTSSSSGLGEE 706

QY 721 PPALPKILLSGSCRADIGCKNSTYDELHVAPL 752

XX



Db 707 PPALPSKLLSSGCKADLCGRSTYDELHAP 738  
 RESULT 5  
 AAU09953  
 ID AAU09953 standard; Protein; 738 AA.  
 AC AAU09953;  
 XX  
 XX 14-FEB-2002 (first entry)  
 XX  
 XX Human Interleukin 17 (IL-17) receptor like protein substitution #3.  
 XX  
 XX Interleukin 17; IL-17 receptor like protein; immunomodulatory;  
 XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 XX  
 XX Homo sapiens.  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX  
 XX Misc-difference 363  
 XX /label= Ser, Thr, Ala, Cys  
 XX  
 XX WO200168859-A2.  
 XX  
 XX 20-SEP-2001.  
 XX  
 XX 15-MAR-2001; 2001WO-0508678.  
 XX  
 XX 16-MAR-2000; 2000US-189816P.  
 XX 28-NOV-2000; 2000US-0724460.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Jing S;  
 XX  
 XX WPI; 2001-611392/79.  
 XX  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma  
 XX  
 XX Claim 20; Page -: 159pp; English.  
 XX  
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 XX include, for example immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infections (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of similar nucleic acids in samples and identify  
 XX patients needing restorative therapy. The IL17rlp may also be used as  
 XX antigens in the production of antibodies against the proteins and in

CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904),  
 CC and has been created according to information given in claim 20.  
 XX  
 XX Sequence 738 AA;  
 XX  
 XX Query Match 97.1%; Score 3897; DB 22; Length 738;  
 XX Best Local Similarity 97.5%; Pred. No. 0;  
 XX Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
 QY 1 MAPWLOLCVSFFVTVNACLSGSLAVAGSGRGACDTCGRWKAARPLCYANEGVGP 60  
 DB 1 MAPWLOLCVSFFVTVNACLSGSLAVAGSGRGACDTCGRWKAARPLCYANEGVGP 46  
 QY 61 ASRNSGLYNTFFKIDNCTYLNPGKVIADANITISQYACHDQVAVTILMSPGALGIE 120  
 DB 47 ASRNSGLYNTFFKIDNCTYLNPGKVIADANITISQYACHDQVAVTILMSPGALGIE 106  
 QY 121 FLKGFVRVILEELASGRCQOOLILKDPKQLNSFFKRTGMSQPTFLNKKFTDTFKVVPF 180  
 DB 107 FLKGFVRVILEELASGRCQOOLILKDPKQLNSFFKRTGMSQPTFLNKKFTDTFKVVPF 166  
 QY 181 PSIKNESNYHPPFFTRACDILLQPDNLACKPFWKPRNLTISQSDQVSPDPAHPNFG 240  
 DB 167 PSIKNESNYHPPFFTRACDILLQPDNLACKPFWKPRNLTISQSDQVSPDPAHPNFG 226  
 QY 241 FRPFTLYLKLHKGPFKRTCKQBTETTSCLLQNVSPGDIYELVDDNTTRKVMYA 300  
 DB 227 FRPFTLYLKLHKGPFKRTCKQBTETTSCLLQNVSPGDIYELVDDNTTRKVMYA 286  
 QY 301 LKPVHSPWAGPIRAVATVPLVVSATFATLFTVMCKKQDQENIYSHLDESSSESTYTA 360  
 DB 287 LKPVHSPWAGPIRAVATVPLVVSATFATLFTVMCKKQDQENIYSHLDESSSESTYTA 346  
 QY 361 LPRRLRPRKPVFLCYSSSDQGNMNVVQCFAFYFLQDFCGCEVALDWEFSLCREGORE 420  
 DB 347 LPRRLRPRKPVFLCYSSSDQGNMNVVQCFAFYFLQDFCGCEVALDWEFSLCREGORE 406  
 QY 421 WYIOKIHESOFILVVCCKMKTFFDKKYNKKGSGKGLFVAVSAIAEKLRAQK 480  
 DB 407 WYIOKIHESOFILVVCCKMKTFFDKKYNKKGSGKGLFVAVSAIAEKLRAQK 466  
 QY 481 SSSAALSKFTANTFDYSCGDVPGILDLSTKTYELMDNLPQLCSHLHSDHGLQEPQHTR 540  
 DB 467 SSSAALSKFTANTFDYSCGDVPGILDLSTKTYELMDNLPQLCSHLHSDHGLQEPQHTR 526  
 QY 541 QGSRNTRFSKSGSLTYVAICNMHOFIDEPDMFQFVPPHPPPLNRYEPVLEKFDGSL 600  
 DB 527 QGSRNTRFSKSGSLTYVAICNMHOFIDEPDMFQFVPPHPPPLNRYEPVLEKFDGSL 586  
 QY 601 VLNDVCKPKGPDSCFLKVEAAVAVGATGPADQSHQSGHGLDQGEARPAIDGSAALQPL 660  
 DB 587 VLNDVCKPKGPDSCFLKVEAAVAVGATGPADQSHQSGHGLDQGEARPAIDGSAALQPL 646  
 QY 661 LHTVKAQSPDMRDSGIYDSSVPSLSLPIAMGSLTDQETTSLSYSSSSGSGGEE 720  
 DB 647 LHTVKAQSPDMRDSGIYDSSVPSLSLPIAMGSLTDQETTSLSYSSSSGSGGEE 706  
 QY 721 PPALPSKLLSSGCKADLCGRSTYDELHAP 752  
 DB 707 PPALPSKLLSSGCKADLCGRSTYDELHAP 738  
 RESULT 6  
 AAU09954  
 ID AAU09954 standard; Protein; 738 AA.  
 AC AAU09954;  
 XX  
 XX 14-FEB-2002 (first entry)



XX Human Interleukin 17 (hIL-17) receptor like protein substitution #4.  
DE Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
DE anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
XX mucin.  
OS Homo sapiens.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Misc-difference 374  
FT /label= Val, Ile, Met, Leu, Phe, Ala, Nle  
XX  
XX WO200168859-A2.  
XX 20-SEP-2001.  
XX 15-MAR-2001; 2001WO-0508678.  
XX 16-MAR-2000; 2000US-199816P.  
XX 28-NOV-2000; 2000US-0724460.  
XX (AMGE-) AMGEN INC.  
XX Jang S;  
XX WPI; 2001-611392/70.  
XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma -  
XX Claim 21; Page 7; 158pp; English.  
XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantify the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17rp may also be used as  
XX antigens in the production of antibodies against the proteins and in  
XX assays to identify modulators of expression and activity. The  
XX anti-IL17rp antibodies and antagonists may also be used to down regulate  
XX expression and activity.  
XX Note: This sequence is not given in the specification but is based on the  
XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
XX and has been created according to information given in claim 21.  
XX Sequence 738 AA;  
XX Query Match 97.1%; Score 3896; DB 22; Length 738;

Best Local Similarity		97.5%;	Pred. No. 0;	Matches		733; Conservative	1; Mismatches	4; Indels	14; Gaps	1;
Qy	1	MAMFQLQSVFTVAC	NGSGLA	VAGSGR	AGADTC	GNRKA	AAAPR	ICLVAN	GVGP	60
Db	1	MAMFQLQSVFTVAC	NGSGLA	VAGSGR	AGADTC	GNRKA	AAAPR	ICLVAN	GVGP	46
Qy	61	ASNSGLNITFYND	CTTLYN	PGKHV	IAQAQ	HTISQ	YACHD	QVAVT	ILMSG	120
Db	47	ASNSGLNITFYND	CTTLYN	PGKHV	IAQAQ	HTISQ	YACHD	QVAVT	ILMSG	106
Qy	121	FLKGFVILEEL	SEGRCQ	QQLIL	KDPK	LNLSF	KRTG	MSQFF	LNNK	180
Db	107	FLKGFVILEEL	SEGRCQ	QQLIL	KDPK	LNLSF	KRTG	MSQFF	LNNK	166
Qy	181	PSIKESNTHP	FFETRAC	DLLLO	PNLAC	PPKPN	LNLSH	OGSD	MOVS	240
Db	167	PSIKESNTHP	FFETRAC	DLLLO	PNLAC	PPKPN	LNLSH	OGSD	MOVS	226
Qy	241	FRFFLYLKL	HEGPF	FRKTC	ROQT	TETTS	CLLON	VSPO	YIEL	300
Db	227	FRFFLYLKL	HEGPF	FRKTC	ROQT	TETTS	CLLON	VSPO	YIEL	286
Qy	301	LKPVHSPW	AGPIRA	VATV	PLVY	ISAF	ATLFT	VMCR	KQENI	360
Db	287	LKPVHSPW	AGPIRA	VATV	PLVY	ISAF	ATLFT	VMCR	KQENI	346
Qy	361	LPRELRPR	PRKVF	LCYSS	KDQNH	NVQC	FAYF	LQDF	CGCE	420
Db	347	LPRELRPR	PRKVF	LCYSS	KDQNH	NVQC	FAYF	LQDF	CGCE	406
Qy	421	WVTKIHES	OFIIV	CVSK	GMKY	FVDK	KNTK	HKG	GRSG	480
Db	407	WVTKIHES	OFIIV	CVSK	GMKY	FVDK	KNTK	HKG	GRSG	466
Qy	481	SSSALSLF	AVYED	SCED	YVGL	DLST	KYK	LYL	MDNL	540
Db	467	SSSALSLF	AVYED	SCED	YVGL	DLST	KYK	LYL	MDNL	526
Qy	541	QGSRRYFR	SRSG	SLFVA	ICN	HOFI	DEEP	DFW	FEKQ	600
Db	527	QGSRRYFR	SRSG	SLFVA	ICN	HOFI	DEEP	DFW	FEKQ	586
Qy	601	VLDNVCKP	GPESD	FC	LKAYE	AVL	GATG	PAD	SDQSH	660
Db	587	VLDNVCKP	GPESD	FC	LKAYE	AVL	GATG	PAD	SDQSH	646
Qy	661	LHTVAGSP	DMPR	DSG	IVD	SSV	SPSS	LSL	PLME	720
Db	647	LHTVAGSP	DMPR	DSG	IVD	SSV	SPSS	LSL	PLME	706
Qy	721	PPALPSKLL	SSGCK	ADG	CRST	YDEL	HA	VAP	752	
Db	707	PPALPSKLL	SSGCK	ADG	CRST	YDEL	HA	VAP	738	

RESULT 7  
AAU09951  
ID AAU09951 standard; Protein; 738 AA.  
XX  
XX AAU09951;  
XX  
DT 14-FEB-2002 (first entry)  
XX Human Interleukin 17 (hIL-17) receptor like protein substitution #1.  
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;

muteln.  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
XX Misc-difference 45 /label= Gly, Pro or Ala  
XX FT  
XX PN W0200168859-A2.  
XX PD 20-SEP-2001.  
XX PF 15-NAR-2001; 2001WO-0508678.  
XX PR 16-NAR-2000; 2000US-189816P.  
XX PR 28-NOV-2000; 2000US-0724460.  
XX PA (ANGE-); AMGEN, INC.  
XX FI Jing, S.;  
XX WPI; 2001-611392/70.  
XX  
XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma  
XX Claim 18; Page 1; 158pp; English.  
XX  
XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-leukemic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantify the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17rlp may also be used as  
XX antigens in the production of antibodies against the proteins and in  
XX assays to identify modulators of expression and activity. The  
XX anti-IL17rlp antibodies and antagonists may also be used to down regulate  
XX expression and activity.  
XX Note: This sequence is not given in the specification but is based on the  
XX human Interleukin 17 (IL-17) receptor like protein sequence (AA093904)  
XX and has been created according to information given in Claim 18.  
XX  
XX Sequence 738 AA;

Query Match 97.0%; Score 3894; DB 22; Length 738;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
QY 1 MAPVQLCSVFTVNAAGGSLAAGGSGRAGADTCGMKMAAARPLCVANEGVP 60  
Db 1 MAPVQLCSVFTVNAAGGSLAAGGSGRAGADTCGMKMAAARPLCVANEGVP 60  
QY 61 ASRNSGLNITFTYDNTCTTLPVKGKRVIAADQNTTISQYACHDQVAVTILWSPGALGTE 120  
Db 47 ASRNSGLNITFTYDNTCTTLPVKGKRVIAADQNTTISQYACHDQVAVTILWSPGALGTE 106

QY 121 FLKGRVILBELASGRQCOQLILKDPKQNSFKTGMESQPLNKKFETDFVKVVPF 180  
Db 107 FLKGRVILBELASGRQCOQLILKDPKQNSFKTGMESQPLNKKFETDFVKVVPF 166  
QY 181 PSIKNESNYHFFFRTRACDILLOPDNLACKPFWKPRNLINISQSGSDQMSYDFDAPHNFG 240  
Db 167 PSIKNESNYHFFFRTRACDILLOPDNLACKPFWKPRNLINISQSGSDQMSYDFDAPHNFG 226  
QY 241 PRFFLYHKLKHSPPKRTCKQBOETTETSCLLQNSVPGDYIIELVDDNTTRKVMYA 300  
Db 227 PRFFLYHKLKHSPPKRTCKQBOETTETSCLLQNSVPGDYIIELVDDNTTRKVMYA 286  
QY 301 LKPVSWAGPIRAVAITVPLVWISAFATLFTVCKRKKQENIYSHLDESSSESTYTA 360  
Db 287 LKPVSWAGPIRAVAITVPLVWISAFATLFTVCKRKKQENIYSHLDESSSESTYTA 346  
QY 361 LPRELPRPKVFLCYSSKQGNHNVVQCFAFYADFGCGCEVALDLWEDFSLCREGORE 420  
Db 347 LPRELPRPKVFLCYSSKQGNHNVVQCFAFYADFGCGCEVALDLWEDFSLCREGORE 406  
QY 421 WYQKIHESQFIIVVCSKGMKFFVDKNTKHKGGGSGKGELEFLVAVSAIAEKLROAKQ 480  
Db 407 WYQKIHESQFIIVVCSKGMKFFVDKNTKHKGGGSGKGELEFLVAVSAIAEKLROAKQ 466  
QY 481 SSSAALSKFTAVTFQYSCGDVPGTLDLSTKYLMDNLPOLCSHLRSRDHGLQEPQHT 540  
Db 467 SSSAALSKFTAVTFQYSCGDVPGTLDLSTKYLMDNLPOLCSHLRSRDHGLQEPQHT 526  
QY 541 QGSRNTRFKSGRSIYVAICNMQFTDEPDHFKQFVPPHPPPLRYEPVLEKFDGSL 600  
Db 527 QGSRNTRFKSGRSIYVAICNMQFTDEPDHFKQFVPPHPPPLRYEPVLEKFDGSL 586  
QY 601 VLNDVCKPGPESDFCLKVEAVLGTGATPADSOSQHGGLDQDGEARPALDGSAAIQL 660  
Db 587 VLNDVCKPGPESDFCLKVEAVLGTGATPADSOSQHGGLDQDGEARPALDGSAAIQL 646  
QY 661 LHTVKGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSLTESYSSSSGLGEE 720  
Db 647 LHTVKGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSLTESYSSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKADLCRSYTDLHNAVAP 752  
Db 707 PPALPSKLLSSGCKADLCRSYTDLHNAVAP 738  
RESULT 8  
AAU09952  
ID AAU09952 standard; Protein; 738 AA.  
XX  
XX AC AAU09952;  
XX  
XX DT 14-FEB-2002 (first entry)  
XX  
XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #2.  
XX  
XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
KW muteln.  
XX  
XX OS Homo sapiens.  
OS Synthetic.  
XX  
XX PH Key Location/Qualifiers  
XX Misc-difference 227 /label= Phe, Leu, Val, Ile, Ala, Tyr  
XX  
XX FT  
XX PN W0200168859-A2.

XX PD 20-SEP-2001.  
 XX PF 15-MAR-2001; 2001WO-US08678.  
 XX PR 16-MAR-2000; 2000US-189816P.  
 XX PR 28-NOV-2000; 2000US-0724460.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Jlog S;  
 XX DR WPI; 2001-611392/70.  
 XX PT Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX PT diabetes, psoriasis and glaucoma  
 XX PS Claim 19; Page : 158pp; English.  
 XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-asthmatic, dermatological,  
 CC anti-parkinsonian, anti-convulsant, anti-leukaemic, anti-infertility and  
 CC osteopathic, vascular, cyostatic, anti-leukaemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rp antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 19.  
 XX CC  
 XX SQ Sequence 738 AA:  
 Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
 QY 1 MAPHLQCSVFETVACVINGSLAVAGCGSGARGADTCGRKAAARPLCVANEGVGP 60  
 DB 1 MAPHLQCSVFETVACVINGSLAVAGCGSGARGADTCGRKAAARPLCVANEGVGP 46  
 QY 61 ASRNSGLNITFKYDNCVTYLPVGRKEVITADQNTISQYACHQVAVTILWSPCALGIE 120  
 DB 47 ASRNSGLNITFKYDNCVTYLPVGRKEVITADQNTISQYACHQVAVTILWSPCALGIE 106  
 QY 121 FLAGFRVILEELKSGRCQQLILKDPKOLNSSFKRTGMSQPLFANKFETDYFVKVVPF 180  
 DB 107 FLAGFRVILEELKSGRCQQLILKDPKOLNSSFKRTGMSQPLFANKFETDYFVKVVPF 166  
 QY 181 PSTKNSNTHPEFFTRACDLLOPNLACKPFRPNLNLISQSGSDQVSDHAPNFG 240  
 DB 167 PSTKNSNTHPEFFTRACDLLOPNLACKPFRPNLNLISQSGSDQVSDHAPNFG 226  
 QY 241 PRFFYHLKHEGPFKRTCKEQETTTSCLLQNVSPGDIIELVDDTNTTRKVHYA 300

DB 227 XRFYLYLKLHEGPFKRTCKEQETTTSCLLQNVSPGDIIELVDDTNTTRKVHYA 286  
 QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVCRKQKQENIYSHLDESSSYTAA 360  
 DB 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVCRKQKQENIYSHLDESSSYTAA 346  
 QY 361 LPRERLRPRKRYFLCTYCKDQNHMMNVVOCFAIFLQDFCGCEVALDLMEDFSLCRGQRE 420  
 DB 347 LPRERLRPRKRYFLCTYCKDQNHMMNVVOCFAIFLQDFCGCEVALDLMEDFSLCRGQRE 406  
 QY 421 WYQKIHESQFLLVYVCKGKRYFVDKNTKHKGGGSGKRGELFVAVSAEKLROAKQ 480  
 DB 407 WYQKIHESQFLLVYVCKGKRYFVDKNTKHKGGGSGKRGELFVAVSAEKLROAKQ 466  
 QY 481 SSSAALSKEFIAYFDYCEGDVPGILDSTKYRLMDNLPCLSHLSDHGLQPGQETR 540  
 DB 467 SSSAALSKEFIAYFDYCEGDVPGILDSTKYRLMDNLPCLSHLSDHGLQPGQETR 526  
 QY 541 QGSRNRYFESGSLVAVCNHGFIDEEDPWEKOFVFPHPPLRYREPTLEKDSGL 600  
 DB 527 QGSRNRYFESGSLVAVCNHGFIDEEDPWEKOFVFPHPPLRYREPTLEKDSGL 586  
 QY 601 VLMDVCKPGPESDFCLKVEAPVILGATGPADSOHESQHGGLDGDGEARPALDGSAALOPL 660  
 DB 587 VLMDVCKPGPESDFCLKVEAPVILGATGPADSOHESQHGGLDGDGEARPALDGSAALOPL 646  
 QY 661 LHTRVAGSPDMPRDSGIYDSSVPSSELSLPLMBGLSTDTQETSSITSVSSSGLGEE 720  
 DB 647 LHTRVAGSPDMPRDSGIYDSSVPSSELSLPLMBGLSTDTQETSSITSVSSSGLGEE 706  
 QY 721 PPALPSKLLSSGCKADLGCRTYTDLHAVAP 752  
 DB 707 PPALPSKLLSSGCKADLGCRTYTDLHAVAP 738  
 RESULT: 9  
 AAU09956  
 ID AAU09956 standard; Protein; 738 AA.  
 XX AC AAU09956;  
 XX DT 14-FEB-2002 (first entry)  
 XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.  
 XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cyostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW muteln.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX FH  
 FT Key Location/Qualifiers  
 FT Misc-difference 515 /Label= Asp, Glu  
 XX PN W0200168859-A2.  
 XX PD 20-SEP-2001.  
 XX PF 15-MAR-2001; 2001WO-US08678.  
 XX PR 16-MAR-2000; 2000US-189816P.  
 XX PR 28-NOV-2000; 2000US-0724460.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI

PI Jing S;  
 XX WPI: 2001-611392/70.  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma  
 XX Claim 23: Page -: 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 XX anti-parkinsonian, anti-convulsant, anti-leukemic, dermatological,  
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
 XX include, for example, immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infectious (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of similar nucleic acids in samples and identify  
 XX patients needing restorative therapy. The IL17rp may also be used as  
 XX antigens in the production of antibodies against the proteins and in  
 XX assays to identify modulators of expression and activity. The  
 XX -anti-IL17rp antibodies and antagonists may also be used to down regulate  
 XX expression and activity.

XX Note: This sequence is not given in the specification but is based on the  
 XX human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)  
 XX and has been created according to information given in claim 23.

XX Sequence 738 AA:

Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative: 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWLCVFFVTNACLSQAVAGSSRGADTCGWRKAAARPLCVANEGVCP 60  
 DB 1 MAPWLCVFFVTNACLSQAVAGSSRGADTCGWRKAAARPLCVANEGVCP 60  
 QY 61 ASRNSGLNITFYDNCITLYNPKGVHVIADQNTISQYACHQDVAVTILSPGALGIE 120  
 DB 47 ASRNSGLNITFYDNCITLYNPKGVHVIADQNTISQYACHQDVAVTILSPGALGIE 106  
 QY 121 FLKGRVILEELKSGROCOQILKDPKQLNSSFRTNGESQPLFNKFTDYFKVYVFF 180  
 DB 107 FLKGRVILEELKSGROCOQILKDPKQLNSSFRTNGESQPLFNKFTDYFKVYVFF 166  
 QY 181 PSIKNESNTHFFFRTRACDILLOPNLACKPWPKNLINSQSGDMQVSDHAPNFG 240  
 DB 167 PSIKNESNTHFFFRTRACDILLOPNLACKPWPKNLINSQSGDMQVSDHAPNFG 226  
 QY 241 FRFTLYHKLKHSPPKTKCQQTETTSCLQNVSGDYIIIEVDYDNTNTRKVNHYA 300  
 DB 227 FRFTLYHKLKHSPPKTKCQQTETTSCLQNVSGDYIIIEVDYDNTNTRKVNHYA 286  
 QY 301 LKPVHSPWAGIPRAVITVPLVWISAFATLTVNCRKQKQENIYSHLDEESSSTYAA 360  
 DB 287 LKPVHSPWAGIPRAVITVPLVWISAFATLTVNCRKQKQENIYSHLDEESSSTYAA 346  
 QY 361 LPRRLRPKPVFLCYSSKDGQNMNVVQCFAFLQDFCGCEVALDWEFSLCREGORE 420  
 DB 347 LPRRLRPKPVFLCYSSKDGQNMNVVQCFAFLQDFCGCEVALDWEFSLCREGORE 406

QY 421 WTQKIHESOFIIVCSKGMKTFYDKKNYKHGGGSGKGEFLFVAVSAIAKLRQAKQ 480  
 DB 407 WTQKIHESOFIIVCSKGMKTFYDKKNYKHGGGSGKGEFLFVAVSAIAKLRQAKQ 466  
 QY 481 SSSAALSFKIATVDFYSCGDPVPGILDSTTKYLRADNLPLCSSLHLSRDRGLQEPQOIR 540  
 DB 467 SSSAALSFKIATVDFYSCGDPVPGILDSTTKYLRADNLPLCSSLHLSRDRGLQEPQOIR 526  
 QY 541 QGSRNRTFRSKSRSLTYAICNMHQFIDEPDMFKQFVPPFPPLPYREPVLEKFDGSL 600  
 DB 527 QGSRNRTFRSKSRSLTYAICNMHQFIDEPDMFKQFVPPFPPLPYREPVLEKFDGSL 586  
 QY 601 VLVDMCKCPKPSDFCLKVEAVLGATGADPADSOHESQHGGLDQGEARPALDGSAAQPL 660  
 DB 587 VLVDMCKCPKPSDFCLKVEAVLGATGADPADSOHESQHGGLDQGEARPALDGSAAQPL 646  
 QY 661 LHTVAKSPDMRPSGDIYDSVPSSELSLPLMEGLSTDTQETTSLSLTSVSSSGLGEE 720  
 DB 647 LHTVAKSPDMRPSGDIYDSVPSSELSLPLMEGLSTDTQETTSLSLTSVSSSGLGEE 706  
 QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAYAP 752  
 DB 707 PPALPSKLLSSGCKADLCGRSYTDELHAYAP 738

RESULT 10  
 AAU09955  
 ID AAU09955 standard; Protein: 738 AA.  
 AC AAU09955;  
 XX AAU09955;  
 DT 14-FEB-2002 (first entry)  
 XX Human Interleukin 17 (hIL-17) receptor like protein substitution #5.  
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutin.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 385  
 XX /label- Cys, Ser, Ala  
 PN WO200168859-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 15-MAR-2001; 2001WO-US08678.  
 XX  
 PR 16-MAR-2000; 2000US-189816P.  
 PR 28-NOV-2000; 2000US-0724460.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Jing S;  
 XX WPI: 2001-611392/70.  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma  
 XX Claim 22: Page -: 158pp; English.

CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicaemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantify the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17r may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17r antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)  
 CC and has been created according to information given in claim 22.

XX Sequence: 738 AA;

Query Match 96.9%; Score 3890; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPVLQCSVFTVACNLGSLAVAGGSGRARGADTCGWMKAARPRCLVANEVGP 60  
 DB 1 MAPVLQCSVFTVACNLGSLAVAGGSGRANGVDCGR-----GVGP 46  
 QY 61 ASRNSGLYNTKYDNCYTLNPGKHVITADQNTISQACHQVAVTILMSPGALGIE 120  
 DB 47 ASRNSGLYNTKYDNCYTLNPGKHVITADQNTISQACHQVAVTILMSPGALGIE 106  
 QY 121 FLKGFVILEELKSGRCCOOLIKDPKOLNSFKRTGMSQPFLLNKKFTDYFKVVPF 180  
 DB 107 FLKGFVILEELKSGRCCOOLIKDPKOLNSFKRTGMSQPFLLNKKFTDYFKVVPF 166  
 QY 181 PSIKNESYHPFFFTACDLLOPDLNCKPFWKPRNLISQBSGMQVSDHAPNFG 240  
 DB 167 PSIKNESYHPFFFTACDLLOPDLNCKPFWKPRNLISQBSGMQVSDHAPNFG 226  
 QY 241 FRFFLYLKLKHEGFKETCKOETETSCLLQNVSPGDIYIELVDNTNTRKVHYA 300  
 DB 227 FRFFLYLKLKHEGFKETCKOETETSCLLQNVSPGDIYIELVDNTNTRKVHYA 286  
 QY 301 LKPVHSPAGTRAVATVPLVWISAFATLFTVMCRKQENIYSHLDESSSTTAA 360  
 DB 287 LKPVHSPAGTRAVATVPLVWISAFATLFTVMCRKQENIYSHLDESSSTTAA 346  
 QY 361 LPRERLPRKPVFLCYTSKQGNHNVVOCFAIFLQDPCGEVALOLWEDFSLREGORE 420  
 DB 347 LPRERLPRKPVFLCYTSKQGNHNVVOCFAIFLQDPCGEVALOLWEDFSLREGORE 406  
 QY 421 WVIQKHESQFIIVCSGKNKIFVDKNTKHGGSGGSGELFVAVSAIAEKLRAKQ 480  
 DB 407 WVIQKHESQFIIVCSGKNKIFVDKNTKHGGSGGSGELFVAVSAIAEKLRAKQ 466  
 QY 481 SSSAALSKFATVFDYCEGVPGLDLSTKTKYRMDNLPOLCSHLHSRDRHQLQEPGQHT 540  
 DB 467 SSSAALSKFATVFDYCEGVPGLDLSTKTKYRMDNLPOLCSHLHSRDRHQLQEPGQHT 526  
 QY 541 QGSRNTFRSKSGRSLTYAICNHQFIIDEPDWFKEKQFVFPFPPPLRYEPVLEKFDGSL 600

DB 527 QGSRNTFRSKSGRSLTYAICNHQFIIDEPDWFKEKQFVFPFPPPLRYEPVLEKFDGSL 586  
 QY 601 VLNDVCKPSPESDFCLKVAZVAVLGATGPASQHSQSGGLDQDGEARPALDGSALQPL 660  
 DB 587 VLNDVCKPSPESDFCLKVAZVAVLGATGPASQHSQSGGLDQDGEARPALDGSALQPL 646  
 QY 661 LHTVKAQSPDMRDSQGIYDSSVPSSELSLPLMSEGLSTDTSTSSVSSSSGLGEE 720  
 DB 647 LHTVKAQSPDMRDSQGIYDSSVPSSELSLPLMSEGLSTDTSTSSVSSSSGLGEE 706  
 QY 721 PPALPSKLLSSGCKADLGCRCRSTYDELAVAP 752  
 DB 707 PPALPSKLLSSGCKADLGCRCRSTYDELAVAP 738

RESULT 11

AA009957  
 ID AA009957 standard; Protein; 738 AA.  
 XX  
 AC AA009957;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutin.

OS Homo sapiens.  
 XX Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 602 /label= Cys, Ala, Ser  
 PN WO200168859-A2.  
 XX  
 PD 20-SEP-2001.  
 PF 15-MAR-2001; 2001WO-US08678.  
 XX  
 PR 16-MAR-2000; 2000US-189816P.  
 PR 28-NOV-2000; 2000US-0724460.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI JIng S;  
 PI  
 DR WPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma -  
 XX  
 PS Claim 24; Page : 158pp; English.

CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and

CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone disorders (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rp antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AA00904)  
 CC and has been created according to information given in claim 24.  
 XX  
 SQ Sequence 738 AA;

Query Match 96.9%; Score 3890; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative. 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPNLQVSVFTVNAALNSQLAVAGSGRAGADTCGRMKAAARPLCVANEGVGP 60  
 DB 1 MAPNLQVSVFTVNAALNSQLAVAGSGRAGADTCGRMKAAARPLCVANEGVGP 60  
 QY 61 ASRSLGNTTFKDYNTTLPVCKVVIADQNTISQYACHQVAVTILSPGALGIE 120  
 DB 47 ASRSLGNTTFKDYNTTLPVCKVVIADQNTISQYACHQVAVTILSPGALGIE 106  
 QY 121 FLKGRVILELSEGRQCOQLILADPKQINSFKTKGSGQPLFMKFTDYFKVYVF 180  
 DB 107 FLKGRVILELSEGRQCOQLILADPKQINSFKTKGSGQPLFMKFTDYFKVYVF 166  
 QY 181 PSIKNESYHFFTRACDILLQPDNLACKPFWKPRNLTISQSGDMQVDFBAPHNFG 240  
 DB 167 PSIKNESYHFFTRACDILLQPDNLACKPFWKPRNLTISQSGDMQVDFBAPHNFG 226  
 QY 241 FFYFLYALKHSGPKRCKQEQTTETTSCLLQNVSPGDIYIELVDNTTKVMYIA 300  
 DB 227 FFYFLYALKHSGPKRCKQEQTTETTSCLLQNVSPGDIYIELVDNTTKVMYIA 286  
 QY 301 LAPVESPWAGPIRAVAITVPLVISAFAITLVKCRKQENITSHLDESSSTYTA 360  
 DB 287 LAPVESPWAGPIRAVAITVPLVISAFAITLVKCRKQENITSHLDESSSTYTA 346  
 QY 361 LREELRPKRVPLCTSSKQGNHNVVQCFATFDQFCGEVALDLDWEDFSLCRGORE 420  
 DB 347 LREELRPKRVPLCTSSKQGNHNVVQCFATFDQFCGEVALDLDWEDFSLCRGORE 406  
 QY 421 WYQIKHESOFIIVVCKGMKYFDKKNYKHGGGSGKGKGLFVAVSAIAEKLQAKQ 480  
 DB 407 WYQIKHESOFIIVVCKGMKYFDKKNYKHGGGSGKGKGLFVAVSAIAEKLQAKQ 466  
 QY 481 SSSAALSKEFIAVFDYSCGDVPGILDLSTKYRLMDNLPCLCSHLHSDRGDLPQHT 540  
 DB 467 SSSAALSKEFIAVFDYSCGDVPGILDLSTKYRLMDNLPCLCSHLHSDRGDLPQHT 526  
 QY 541 QGSRNTFRSKSGSLVAVCNHGFIDEEDPFKQFVPPHPPPLRYREPLVLEFDSL 600  
 DB 527 QGSRNTFRSKSGSLVAVCNHGFIDEEDPFKQFVPPHPPPLRYREPLVLEFDSL 586  
 QY 601 VLNDVCKPSPESDFCLKYEAATVATGATGPADSDQSHSQHGLDQDGEARPALDGAALQPL 660  
 DB 587 VLNDVCKPSPESDFCLKYEAATVATGATGPADSDQSHSQHGLDQDGEARPALDGAALQPL 646  
 QY 661 LETVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDTQETSLATESVSSSGIGEE 720  
 DB 647 LETVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDTQETSLATESVSSSGIGEE 706

QY 721 PPALPSKLLSSGSKRADIGCRSYTDELHAVAP 752  
 DB 707 PPALPSKLLSSGSKRADIGCRSYTDELHAVAP 738

RESULT 12

AA011355

ID AA011355 standard; Protein; 738 AA.

AC AA011355;

DT 26-MAR-2002 (first entry)

DE Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.

KW Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;

KW gene therapy; protein therapy; immunological disorder.

OS Homo sapiens.

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Db 47 ASRNSGLNITFKYDNCITLNPVGRKHVTAQAQNTISYQACHQDVAVITLWSPALGIE 106  
 QY 121 FLAGFVILEELKSGROCOOLILKDKPKNLSKFRKMGESQEPFLNMFETDIYVKKVVP 180  
 Db 107 FLAGFVILEELKSGROCOOLILKDKPKNLSKFRKMGESQEPFLNMFETDIYVLR-LSF 165  
 QY 181 PSIKNSNTHPFFTRACDLLOPDLACFPKPKPRNLISOGSDMOVSFDRAPNFC 240  
 Db 166 SPINKNSNTHPFFTRACDLLOPDLACFPKPRNLISOGSDMOVSFDRAPNFC 225  
 QY 241 FRFTLHYLKLKHEGPKFKCKOETTTSCLLQNVSPGDYIIEIWDVNTTRVHYA 300  
 Db 226 FRFTLHYLKLKHEGPKFKCKOETTTSCLLQNVSPGDYIIEIWDVNTTRVHYA 285  
 QY 301 LKPVHSPHAGPTRAIVATVPLVISAFTLVWCRKQKQNIYSHLDEESSESTTAA 360  
 Db 286 LKPVHSPHAGPTRAIVATVPLVISAFTLVWCRKQKQNIYSHLDEESSESTTAA 345  
 QY 361 LPRRLRPKPVLCYSSKDGONNNVQCFATFLQDFCCGCEVALDLDNEDSLCRGORE 420  
 Db 346 LPRRLRPKPVLCYSSKDGONNNVQCFATFLQDFCCGCEVALDLDNEDSLCRGORE 405  
 QY 421 WVIQKHESQFIIIVCSGKMYFVDKNTKKGGRSGKGLFLVAVSATAELKRAQK 480  
 Db 406 WVIQKHESQFIIIVCSGKMYFVDKNTKKGGRSGKGLFLVAVSATAELKRAQK 465  
 QY 481 SSSAALSKFIATYDYSCEGDPVGIILDLSTKYLMDNLPLQCLSHLSRDHGLQPGQTR 540  
 Db 466 SSSAALSKFIATYDYSCEGDPVGIILDLSTKYLMDNLPLQCLSHLSRDHGLQPGQTR 525  
 QY 541 QGSRNRYFSKGRSLYVACNMQFIIDEPWFKEQFVFPHPPLRYREPVLKFDGSL 600  
 Db 526 QGSRNRYFSKGRSLYVACNMQFIIDEPWFKEQFVFPHPPLRYREPVLKFDGSL 585  
 QY 601 VLNDVCKPGPESDCLAVEAVLGATGPADSOHESQGLDQDGEARPLDGSNAQPL 660  
 Db 586 VLNDVCKPGPESDCLAVEAVLGATGPADSOHESQGLDQDGEARPLDGSNAQPL 645  
 QY 661 LHTVKGSPDMPGSDYDSSVPSSELSPLMBCLSTDTOTETSSLTSSVSSSGLGE 720  
 Db 646 LHTVKGSPDMPGSDYDSSVPSSELSPLMBCLSTDTOTETSSLTSSVSSSGLGE 705  
 QY 721 PPALPSKLLSSGCRADIGCRSTYDELHVAPL 753  
 Db 706 PPALPSKLLSSGCRADIGCRSTYDELHVAPL 738

RESULT 13  
 AAU04958  
 ID AAU04958 standard; Protein; 728 AA.  
 AC AAU04958;  
 XX AAU04958;  
 DT 24-OCT-2001 (first entry)  
 XX Human Interleukin-17 receptor, IL-17RH4.  
 KW Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;  
 KW PRO20026; DNA 154095-2998; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 OS Homo sapiens.  
 FH Key: Location/Qualifiers  
 FT Region 19..24  
 FT /note= "N-myristoylation site"  
 FT Modified-site 31..34  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 38..41  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 56..59

FT Modified-site /note= "Asn is N-glycosylated"  
 FT 113..116  
 FT /note= "Asn is N-glycosylated"  
 FT 147..150  
 FT /note= "Asn is N-glycosylated"  
 FT 182..185  
 FT /note= "Asn is N-glycosylated"  
 FT 232..235  
 FT /note= "cAMP/GMP-dependent protein kinase  
 FT phosphorylation site"  
 FT 266..269  
 FT /note= "Asn is N-glycosylated"  
 FT 283..307  
 FT /note= "Transmembrane domain"  
 FT 312..319  
 FT /note= "Tyrosine kinase phosphorylation site"  
 FT 375..380  
 FT /note= "N-myristoylation site"  
 FT 416..424  
 FT /note= "Tyrosine kinase phosphorylation site"  
 FT 428..433  
 FT /note= "N-myristoylation site"  
 FT 429..434  
 FT /note= "N-myristoylation site"  
 FT 432..437  
 FT /note= "N-myristoylation site"  
 FT 433..436  
 FT /note= "Glycosaminoglycan attachment site"  
 FT 517..522  
 FT /note= "N-myristoylation site"  
 FT 574..579  
 FT /note= "N-myristoylation site"  
 FT 652..657  
 FT /note= "N-myristoylation site"  
 FT 707..712  
 FT /note= "N-myristoylation site"  
 XX W0200146420-A2.  
 XX 28-JUN-2001.  
 XX 20-DEC-2000; 2000MO-US34956.  
 XX 23-DEC-1999; 99US-0172096.  
 XX 30-DEC-1999; 99MO-US31274.  
 XX 11-JAN-2000; 2000US-0175481.  
 XX 18-FEB-2000; 2000MO-US04341.  
 XX 02-MAR-2000; 2000MO-US05841.  
 XX 21-MAR-2000; 2000US-0191007.  
 XX 21-MAR-2000; 2000MO-US07532.  
 XX 02-JUN-2000; 2000MO-US15264.  
 XX 22-JUN-2000; 2000US-0213087.  
 XX 22-AUG-2000; 2000US-0844848.  
 XX 24-AUG-2000; 2000MO-US23328.  
 XX 24-OCT-2000; 2000US-0242837.  
 XX 10-NOV-2000; 2000MO-US30873.  
 XX 28-NOV-2000; 2000US-0253646.  
 XX 01-DEC-2000; 2000MO-US32678.  
 XX (GETH ) GENENTECH INC.  
 XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RL;  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;  
 XX WPI: 2001-451708/48.  
 XX N-PSDB; AAS09517.  
 XX Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes  
 XX Claim 10; Fig 18; 188pp; English.



XX The sequence is PRO20026 which is the human Interleukin 17 receptor,  
CC IL-17RA, encoded by DNA 154095-2998. A composition  
CC containing ant/agonists to the PRO polypeptides or individual components  
CC are useful for treating a mammal with an immune related disease, e.g.  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic inflammatory myopathy, Sjogren's syndrome, systemic  
CC scleroderma, autoimmune haemolytic anaemia, autoimmune renal  
CC vasculitis, sarcoidosis, thyroiditis, diabetes mellitus, immune-mediated skin  
CC disease, contact dermatitis, an allergic disease e.g. food  
CC disease, chronic inflammatory disease, a transplant associated disease, or a  
CC chronic inflammatory disease, a transplant associated disease, or a  
CC hypersensitivity, asthma, a transplant associated disease, or a  
CC degenerative cartilaginous disorder comprising administering a PRO1031 or  
CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
CC examples of the diseases and disorders are given in the specification.  
XX Sequence 728 AA;

Query Match 92.3%; Score 3703; DB: 22; Length 728;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RKMAARPRCLVANE-GVGPASRNSGLYNTFFKIDNCTYLMVPGKHVIADQNTISQY 100  
Db 3 RASAGVPALFVSGGVGPASRNSGLYNTFFKIDNCTYLMVPGKHVIADQNTISQY 62  
QY 101 ACHDQVAVTILWSPGALGIEFLKFRVILEELKSGROCOOLILKDPKQLNSFKRTGHE 160  
Db 63 ACHDQVAVTILWSPGALGIEFLKFRVILEELKSGROCOOLILKDPKQLNSFKRTGHE 122  
QY 161 SOPFLNKKFTDFVAVVDFPSIKNESNYHFFFRACDILLOPNLACKPFRNIN 220  
Db 123 SOPFLNKKFTDFVAVVDFPSIKNESNYHFFFRACDILLOPNLACKPFRNIN 182  
QY 221 ISQ-----HGSDQVSPFDHAPNFGFRFFLHLKHEGFFKTKCOEQTT 267  
Db 183 ISQSGSDQVSPFDHAPNFGFRFFLHLKHEGFFKTKCOEQTT 242  
QY 268 ETISCLLQNSVPGDYIELVDVDTNTRVVMYALKPVHSPWAGPIRAVITVPLVVISAF 327  
Db 243 ETISCLLQNSVPGDYIELVDVDTNTRVVMYALKPVHSPWAGPIRAVITVPLVVISAF 302  
QY 328 ATLETVMCRKQCOENIYSHLDEESSESTYTAALPRERLRPRKPVFLCYSSKDGQNHNV 387  
Db 303 ATLETVMCRKQCOENIYSHLDEESSESTYTAALPRERLRPRKPVFLCYSSKDGQNHNV 362  
QY 388 VQCFATFLQPCGCEVALDWEISLCRGOREWVQKTHESQFIIVVCSGKMYFVDRK 447  
Db 363 VQCFATFLQPCGCEVALDWEISLCRGOREWVQKTHESQFIIVVCSGKMYFVDRK 422  
QY 448 NTKHGGGSGGSGELFVAVSAIAELKQAKOSSAALSFIAYFYDYSCGDVPGILD 507  
Db 423 NTKHGGGSGGSGELFVAVSAIAELKQAKOSSAALSFIAYFYDYSCGDVPGILD 482  
QY 508 LSTYRLMDLNPOLCSHLSRDLGLOEPGQHTQSGSRNFRSKSGSLVAVICNNHQFI 567  
Db 483 LSTYRLMDLNPOLCSHLSRDLGLOEPGQHTQSGSRNFRSKSGSLVAVICNNHQFI 542  
QY 568 DEEDPWEKQFVFPFPPPLRYRPEVLEKFDGSLVNDVCKPDPSPDFCLVAVIGAT 627  
Db 543 DEEDPWEKQFVFPFPPPLRYRPEVLEKFDGSLVNDVCKPDPSPDFCLVAVIGAT 602  
QY 628 GPASQSHSGGGLDQDGRAPALDGSAAQLPILHTVAGSPDMRDXGIDYSSVPSSE 687  
Db 603 GPASQSHSGGGLDQDGRAPALDGSAAQLPILHTVAGSPDMRDXGIDYSSVPSSE 662  
QY 688 LSLPLMGLSTDTTSSITSVSSSSGLGEPPPALPSKLLSGSKADLGCSTYDEL 747  
Db 663 LSLPLMGLSTDTTSSITSVSSSSGLGEPPPALPSKLLSGSKADLGCSTYDEL 722  
QY 748 HAVAPL 753

Db 723 HAVAPL 728  
RESULT 14  
AAU10602  
ID AAU10602 standard; Protein; 739 AA.  
XX AAU10602;  
XX 14-FEB-2002 (first entry)  
XX Human Interleukin 17 (hIL-1) receptor-like protein version 2.  
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
XX vascular; cycostatic; anti-leukaemic; anti-inferility; ophthalmological;  
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
XX bone disease; vascular disorder; eye disorder; cancer; human.  
XX Homo sapiens.  
XX WO200168859-A2.  
XX 20-SEP-2001.  
XX 15-MAR-2001; 2001WO-US08678.  
XX 16-MAR-2000; 2000US-189816P.  
XX 28-NOV-2000; 2000US-0724460.  
XX (AMGE-) AMGEN INC.  
XX Jibg S;  
XX WPI; 2001-611392/70.  
XX N-PSDB; AAS16201.  
XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,  
XX diabetes, psoriasis and glaucoma.  
XX Claim 2; Fig 1; 158pp; English.  
XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cycostatic, anti-leukaemic, anti-inferility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema) skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukaemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantitate the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17rlp may also be used as  
XX antigens in the production of antibodies against the proteins and in  
XX assays to identify modulators of expression and activity. The  
XX anti-IL17rlp antibodies and antagonists may also be used to down regulate  
XX expression and activity. This is the amino acid sequence of human  
XX Interleukin 17 (IL-17) receptor like protein described in the method of



CC the invention.  
 CC Note: Residues 1-288 of this sequence correspond to residues 8-296 of the  
 CC sequence shown in AU10601 which is incomplete in the specification.  
 XX  
 SQ Sequence 739 AA;

Query Match 92.3%; Score 3703; DB 22; Length 739;  
 Best Local Similarity 93.7%; Pred. No. 0;  
 Matches 704; Conservative 5; Mismatches 22; Indels 20; Gaps 3;  
 QY 3 PMQLQCSVFTTNACLSQSLVAAGSGRAGADTCGRWKAARPRCLVANGSGVGP 62  
 Db 9 PGSQQC-----CLHLDNGLCVG-----RANWLSASC-----LVPPQGVGPAS 48  
 QY 63 RNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQYACHQDVAVTILSPGALGIEFL 122  
 Db 49 RNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQYACHQDVAVTILSPGALGIEFL 108  
 QY 123 KGRVILEELKSGRQCOQLILADPKQLANSFKTGMESOPFLNKKFTDYVTVVPPS 182  
 Db 109 KGRVILEELKSGRQCOQLILADPKQLANSFKTGMESOPFLNKKFTDYVTVVPPS 168  
 QY 183 IKNESNTHFFPTFRACDILQPDNKLACPKPKPRNLNISQHSQDMQVYFDRAPNFR 242  
 Db 169 IKNESNTHFFPTFRACDILQPDNKLACPKPKPRNLNISQHSQDMQVYFDRAPNFR 228  
 QY 243 FFYLHLKLEHGFPRKTKCOBQTTTSCLLQNVSPGDYIIELVDDNTTRKVMHYALK 302  
 Db 229 FFYLHLKLEHGFPRKTKCOBQTTTSCLLQNVSPGDYIIELVDDNTTRKVMHYALK 288  
 QY 303 PVSPWAGPIRAVATVPLVVISAFATLFTVNCRRKQOENIYSHLDESSSSSYTAALP 362  
 Db 289 PVSPWAGPIRAVATVPLVVISAFATLFTVNCRRKQOENIYSHLDESSSSSYTAALP 348  
 QY 363 RERLRPRPVFLCYSSKDGQNNVYOCFAFLQDCGCEVALDLWEDFSLCRGQREW 422  
 Db 349 RERLRPRPVFLCYSSKDGQNNVYOCFAFLQDCGCEVALDLWEDFSLCRGQREW 408  
 QY 423 IQKHESQIIIVVCSKGMVYDKNYHKGSGSGKGLFLVAYSALAKLQAKQSS 482  
 Db 409 IQKHESQIIIVVCSKGMVYDKNYHKGSGSGKGLFLVAYSALAKLQAKQSS 468  
 QY 483 SALSFTIAYFDYSCGSDVPGIILDLSTKYLMLNLPOLCSHLHSRDLGQEPQHTROG 542  
 Db 469 SALSFTIAYFDYSCGSDVPGIILDLSTKYLMLNLPOLCSHLHSRDLGQEPQHTROG 528  
 QY 543 SRNIFRSKSGSLVATCNHOFIDEEDPWFKEQFVFPFPPPLRYRFPVLEKFDGLVL 602  
 Db 529 SRNIFRSKSGSLVATCNHOFIDEEDPWFKEQFVFPFPPPLRYRFPVLEKFDGLVL 588  
 QY 603 NDVNCAPGSDVFLKVAALVATGATPADSQRHSGHGLDQGEARPALDGSALQPLH 662  
 Db 589 NDVNCAPGSDVFLKVAALVATGATPADSQRHSGHGLDQGEARPALDGSALQPLH 648  
 QY 663 TVTAGSPDMPDSDGIYDSSVPSSLSPLMEGLSTDTSTSLTESVSSSGIGREPP 722  
 Db 649 TVTAGSPDMPDSDGIYDSSVPSSLSPLMEGLSTDTSTSLTESVSSSGIGREPP 708  
 QY 723 ALPSKLLSSGSKADIGCRSYTDELHVAPL 753  
 Db 709 ALPSKLLSSGSKADIGCRSYTDELHVAPL 739

RESULT 15  
 ABB07630  
 ID ABB07630 standard; Protein; 739 AA.  
 XX  
 AC ABB07630;  
 XX  
 DT 20-MAY-2002 (first entry)  
 XX  
 DE Murine cytokine receptor, Zcytor18.  
 XX

KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;  
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 KW erythroleukemia; chromosome 3p14.3; gene therapy; mouse.  
 XX  
 OS Mus sp.  
 XX WO200208259-A2.  
 XX  
 XX 31-JAN-2002.  
 XX  
 XX 23-JUL-2001; 2001WO-US23253.  
 XX  
 XX 26-JUL-2000; 2000US-220747P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Presnell SR, Kuestner RE, Gao Z;  
 XX WPI: 2002-217048/77.  
 XX N-PSDB; ABA95037; ABA95038.  
 XX  
 XX New cytokine receptor polypeptide designated zcytor18, useful for  
 XX inhibiting cell proliferation associated with psoriasis or tumor  
 XX growth, and modulating immune system by binding to endogenous zcytor18  
 XX ligand  
 XX  
 XX Claim 1: Page 111-115; 119pp; English.  
 XX  
 XX The invention relates to an isolated cytokine receptor polypeptide  
 XX designated zcytor18. The zcytor18 polypeptides can be expressed by  
 XX standard recombinant methodology. The polypeptides can be used to inhibit  
 XX cell proliferation associated with psoriasis or tumor growth. The  
 XX encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in  
 XX vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 XX and localize zcytor18 gene expression in tissue samples. The probes are  
 XX also useful for detecting gross aberrations in chromosome 3 in which  
 XX zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 XX linkage-based testing of pulmonary alveolar proteinosis, familial  
 XX periodic fever and erythroleukemia, and erythroleukemia associated with  
 XX polymorphisms of cytokine receptors. The present sequence represents a  
 XX murine zcytor18 amino acid sequence.

Query Match 84.4%; Score 3387; DB 23; Length 739;  
 Best Local Similarity 85.2%; Pred. No. 0;  
 Matches 645; Conservative 37; Mismatches 53; Indels 22; Gaps 6;  
 QY 1 MAPQLQCSVFTTNACLSQSLVAAGSGRAGADTCGRWKAARPRCLVANGSGVGP 60  
 Db 1 MAPQLQCSVFTTNACLSQSLVAAGSGRAGADTCGRWKAARPRCLVANGSGVGP 46  
 QY 61 ASRNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQYACHQDVAVTILSPGALGI 119  
 Db 47 ASRNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQYACHQDVAVTILSPGALGI 106  
 QY 120 EFLKGRPVILEELKSGRQCOQLILADPKQLANSFKTGMESOPFLNKKFTDYFVRYVP 179  
 Db 107 EFLKGRPVILEELKSGRQCOQLILADPKQLANSFKTGMESOPFLNKKFTDYFVRYVP 166  
 QY 180 FPSIKNESNTHFFPTFRACDILQPDNKLACPKPKPRNLNISQHSQDMQVYFDRAPNFR 239  
 Db 167 FPSIKNESNTHFFPTFRACDILQPDNKLACPKPKPRNLNISQHSQDMQVYFDRAPNFR 226  
 QY 240 GFRFFYLHLKLEHGFPRKTKCOBQTTTSCLLQNVSPGDYIIELVDDNTTRKVMHY 299  
 Db 227 GFRFFYLHLKLEHGFPRKTKCOBQTTTSCLLQNVSPGDYIIELVDDNTTRKVMHY 286  
 QY 300 ALKPVSPWAGPIRAVATVPLVVISAFATLFTVNCRRKQOENIYSHLDESSSSSYTA 359  
 Db 287 VKESQSPWAGPIRAVATVPLVVISAFATLFTVNCRRKQOENIYSHLDESSSSSYTA 346

```

QY 360 ALPRRLPRKPYLCYSSKQGNMNVOCFAYFLODCGCEVALDLWEDFSLCHRGQR 419
Db 347 ALPRDLPPQPKVFLCTSNKQGNMNVOCFAYFLODCGCEVALDLWEDFSLCHRGQR 406
QY 420 ENVIQKIHESQFIIVVCSKGMKIFVDRKNNKHGGRSGKGGELFLVAVSAIAEKLRQAK 479
Db 407 ENVIQKIHESQFIIVVCSKGMKIFVDRKNNKHGGRSGKGGELFLVAVSAIAEKLRQAK 466
QY 480 QSSSAALSKFIAYFYDSCGDPGILDLSTKYRLMDNLPOLCSHLHSRDBGLQEP-GQH 538
Db 467 QSSSAALSKFIAYFYDSCGDPGILDLSTKYRLMDNLPOLCSHLHSRDBGLQEP-GQH 523
QY 539 TRQSSRRNIFRSKSGSLVAICNNHOFIDEEPDMFEKQVPPHPPPLRYREPVLKFD 598
Db 524 PGHSSRRNIFRSKSGSLVAICNNHOFIDEEPDMFEKQVPPHPPPRYQEPVLKFD 583
QY 599 GLVNDYMKGPESDPCLVYEAVALGATGPADSOH--ESQHGILDODGEARPDGSA 656
Db 584 GLVNDYMKGPESDPCLVYEAVALGATGPADSOH--ESQHGILDODGEARPDGSA 643
QY 657 LQPLHVTYKAGSDMPDROSGIYDSSVPSSELSPLMBGLSTQDTETSSITESVSSSGL 716
Db 644 LQPLHVTYKAGSDMPDROSGIYDSSVPSSELSPLMBGLSTQDTETSSITESVSSSGL 703
QY 717 GEEPPALPSKLLSGCKADIGCRSYTDELHAPL 753
Db 704 GEEDPPTLPKLPASGVR-BHGCHSHTDELQALAPL 739

```

Search completed: May 19, 2003, 09:20:05  
Job time : 59.6401 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:14:29 ; Search time 32.7919 Seconds

(without alignments)  
2626.495 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_336\_753

Perfect score: 2210

Sequence: 1 RKQOENIYSHLDESSSS.....CFADLCRSTYDELHVAVL 418

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

- 1: SP\_ARCHAEA.\*
- 2: SP\_BACTERIA.\*
- 3: SP\_FUNGI.\*
- 4: SP\_HUMAN.\*
- 5: SP\_INVERTEBRATE.\*
- 6: SP\_MAMMAL.\*
- 7: SP\_MHC.\*
- 8: SP\_ORGANELLE.\*
- 9: SP\_PHAGE.\*
- 10: SP\_PLANT.\*
- 11: SP\_RODENT.\*
- 12: SP\_VIRUS.\*
- 13: SP\_VERTEBRATE.\*
- 14: SP\_UNCLASSIFIED.\*
- 15: SP\_VIRUS.\*
- 16: SP\_BACTERIAP.\*
- 17: SP\_ARCHAEA.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2210	100.0	564	Q9UFA0	Q9UFA0 homo sapien
2	1817.5	82.2	582	Q8R578	Q8R578 mus musculus
3	1065.5	48.2	745	Q8QHJ9	Q8QHJ9 brachydanio
4	1065.5	48.2	745	Q8QHJ6	Q8QHJ6 caenorhabditis
5	150.5	6.8	846	Q9RA64	Q9RA64 caenorhabditis
6	111.5	5.0	348	Q9H460	Q9H460 homo sapien
7	111.5	5.0	370	Q96KN9	Q96KN9 homo sapien
8	110	5.0	428	Q9NTU6	Q9NTU6 homo sapien
9	108	4.9	1058	Q9AY10	Q9AY10 oryza sativ
10	107.5	4.9	3942	Q88737	Q88737 mus musculus
11	107	4.8	1322	Q9QZP6	Q9QZP6 mus musculus
12	105	4.8	757	Q13399	Q13399 ustilago ma
13	105	4.8	901	Q24573	Q24573 drosophila
14	105	4.8	1571	Q54978	Q54978 mus musculus
15	104.5	4.7	707	Q96SK7	Q96SK7 homo sapien
16	102.5	4.6	593	Q99PV2	Q99PV2 rattus norv

#### ALIGNMENTS

##### RESULT 1

Q9UFA0  
ID Q9UFA0 PRELIMINARY; PRT; 564 AA.  
AC Q9UFA0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE Hypothetical 63.1 kDa protein (Fragment).  
GN DKFP434N1928  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RC TISSUE=TESTIS;  
RA Blocher H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,  
RL Wiemann S., Schaeuble C., Schaeuble C., Schaeuble C., Schaeuble C.,  
DR EMBL, AL133097; CAB61408.1;  
KW Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E88C CRC64;

Query Match 100.0%; Score 2210; DB 4; Length 564;  
Best Local Similarity 100.0%; Pred. No. 1.3e-181;  
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKQOENIYSHLDESSSSSTYTAALPRRLPRPKVFLCYSSKQGNHNVVQCFAFL 60  
DB 147 RKQOENIYSHLDESSSSSTYTAALPRRLPRPKVFLCYSSKQGNHNVVQCFAFL 206  
QY 61 QDFCGEVALDWEFSLCREGQREWVIOKIHESQFIIVCSKGNFYFDKNTKHGGG 120  
DB 207 QDFCGEVALDWEFSLCREGQREWVIOKIHESQFIIVCSKGNFYFDKNTKHGGG 266  
QY 121 RGSCKELFLVANSIAIAKLRQAKSSAALSFKTANFYDSCGDPGCLDLSTKRLM 180  
DB 267 RGSCKELFLVANSIAIAKLRQAKSSAALSFKTANFYDSCGDPGCLDLSTKRLM 326

Q9bhw7 leishmania  
Q9n918 leishmania  
Q8tcu4 homo sapien  
Q9n053 macaca fasc  
Q9v490 drosophila  
Q9rnp2 zymomonas m  
Q9ke04 bacillus ha  
Q9v216 homo sapien  
Q93vp4 arabidopsis  
Q9up36 homo sapien  
Q91x42 arabidopsis  
Q9v414 zea mays (m  
Q91ok0 arabidopsis  
Q91e31 arabidopsis  
Q9kxv1 halocynthia  
Q14596 homo sapien  
Q13109 homo sapien  
Q92809 abelsson mur  
Q9m436 homo sapien  
Q9wimo drosophila  
Q91v13 mus musculus  
Q9der4 gallus gall  
Q9bw44 homo sapien  
Q91fz2 arabidopsis  
Q8r0b7 mus musculus  
Q9h119 homo sapien  
Q9h118 homo sapien  
Q9ghr8 homo sapien  
Q13517 homo sapien

QY 181 DNLPLCSHLHSRDLQEPGQHTROGSRNTFRSKSGSLTYAICNNHQFIDEEDPWF 240  
 DB 327 DNLPLCSHLHSRDLQEPGQHTROGSRNTFRSKSGSLTYAICNNHQFIDEEDPWF 386  
 QY 241 KQVFPBPPLRYREPVLKFDGSLVNDVCKPQSPDPCFLKVEAVLGATGPAUSQHE 300  
 DB 387 KQVFPBPPLRYREPVLKFDGSLVNDVCKPQSPDPCFLKVEAVLGATGPAUSQHE 446  
 QY 301 SQGGQDQGEARPAIDGSAALQPLHTVTKAGSPDMPSDGYDSSVPSSELSLPLWEG 360  
 DB 447 SQGGQDQGEARPAIDGSAALQPLHTVTKAGSPDMPSDGYDSSVPSSELSLPLWEG 506  
 QY 361 LSTDOTETSLTSSVSSSGSGEPEPPALPKLLSSGSCADIGCRSTYDELHVAFL 418  
 DB 507 LSTDOTETSLTSSVSSSGSGEPEPPALPKLLSSGSCADIGCRSTYDELHVAFL 564  
 RESULT 2  
 Q8R5J8 PRELIMINARY; PRT; 582 AA.  
 ID Q8R5J8  
 AC Q8R5J8  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Similar expression to FGF protein (fragment).  
 GN SEF.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21824237; PubMed-11802165;  
 RA Furtbauer M., Lin W., Ang J.S.L., Thisse B., Thisse C.;  
 RT "SeF is a feedback-induced antagonist of Ras/MAPK-mediated FGF  
 RT signalling";  
 RL Nat. Cell Biol. 4:170-174(2002).  
 DR ENBL; AF24804; AAL79530.1;  
 FT NON-TER 1;  
 SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268B CRC64;

Query Match 82.2%; Score 1817.5; DB 11; Length 582;  
 Best Local Similarity 83.4%; Pred. No. 8e-148;  
 Matches 351; Conservative 25; Mismatches 38; Indels 7; Gaps 4;  
 QY 1 RKQENIYSHLDESESTYTAALPRERLRPRKPVFLCYSSKDGQNNHNVQCFAYEL 60  
 DB 166 RKQENIYSHLDESESTYTAALPRERLRPRKPVFLCYSSKDGQNNHNVQCFAYEL 225  
 QY 61 QDFCGCEVALDWDGSLCREGQREWVQKIHESQFIIVVCSKGMKIFVDKKNYKKG 120  
 DB 226 QDFCGCEVALDWDGSLCREGQREWVQKIHESQFIIVVCSKGMKIFVDKKNYKKG 285  
 QY 121 RSGKGFVAVASIAEKLRQAKSSAALSKFIATYFDYCEGDVPCILDTKYLRL 180  
 DB 286 RGAQGEFLVAVASIAEKLRQAKSSAALSKFIATYFDYCEGDVPCILDTKYLRL 345  
 QY 181 DNLPLCSHLHSRDLQEPGQHTROGSRNTFRSKSGSLTYAICNNHQFIDEEDPWF 239  
 DB 346 DLPELCAHLHS---GQEVYLGHPCHSSRRNTFRSKSGSLTYAICNNHQFIDEEDPWF 402  
 QY 240 EKQVFPBPPLRYREPVLKFDGSLVNDVCKPQSPDPCFLKVEAVLGATGPAUSQHE 299  
 DB 403 EKQVFPBPPLRYREPVLKFDGSLVNDVCKPQSPDPCFLKVEAVLGATGPAUSQHE 462  
 QY 300 --ESQGGGLDQGEARPAIDGSAALQPLHTVTKAGSPDMPSDGYDSSVPSSELSLPL 357  
 DB 463 YLESQGVGLDQGEARPAIDGSAALQPLHTVTKAGSPDMPSDGYDSSVPSSELSLPL 522  
 QY 358 MEGSLSTQETSSLTSSVSSSGSGEPEPPALPKLLSSGSCADIGCRSTYDELHVAFL 417  
 DB 523 MEGSLSTQETSSLTSSVSSSGSGEPEPPALPKLLSSGSCADIGCRSTYDELHVAFL 581

QY 418 L 418  
 DB 582 L 582  
 RESULT 3  
 Q8QEZ9 PRELIMINARY; PRT; 745 AA.  
 ID Q8QEZ9  
 AC Q8QEZ9  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE SeF.  
 GN SEF.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 CC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21824236; PubMed-11802164;  
 RA Teang M., Friesel R., Kudoh T., David I.;  
 RT "Identification of SeF, a novel modulator of FGF signalling";  
 RL Nat. Cell Biol. 4:165-169(2002).  
 DR ENBL; AF364103; AAL76112.1;  
 SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DB4 CRC64;  
 Query Match 48.2%; Score 1065.5; DB 13; Length 745;  
 Best Local Similarity 52.6%; Pred. No. 5.6e-83;  
 Matches 222; Conservative 63; Mismatches 104; Indels 33; Gaps 7;  
 QY 1 RKQENIYSHLDESESTYTAALPRERLRPRKPVFLCYSSKDGQNNHNVQCFAYEL 60  
 DB 321 RKQENIYSHLDESESTYTAALPRERLRPRKPVFLCYSSKDGQNNHNVQCFAYEL 380  
 QY 61 QDFCGCEVALDWDGSLCREGQREWVQKIHESQFIIVVCSKGMKIFVDKKNYKKG 120  
 DB 381 QDFCGCEVALDWDGSLCREGQREWVQKIHESQFIIVVCSKGMKIFVDKKNYKKG 440  
 QY 121 R-----GSGKGFVAVASIAEKLRQAKSSAALSKFIATYFDYCEGDVPC 169  
 DB 441 KENKREPSADSSSSSSRLDFIVASAIISKEIKYHQKSS-DLSRFMSYFDYSHETDPT 499  
 QY 170 ILDTKYLRLADNLPLCSHLHSRDLQEPGQHTROGSRNTFRSKSGSLTYAICNNH 229  
 DB 500 SLSLAPKFLADQLPLFARLHSRDLSTDRPQPPNWSKRNPCSKSGSLTYAICNNH 559  
 QY 230 QFTDEEPWFQKVPFPPPLRYREPVLKFDGSLVNDVCKPQSPDPCFLKVEAVL 289  
 DB 560 QHTVQEPNLEKELM---PPPLPNRTIPKVDGSLVLEKLVKLGSESE-CPPVRSNVL 615  
 QY 290 -----CATGPADGSEHSGHGLDQGEARPAIDGSAALQPLHTVTKAGSPDMPSD 342  
 DB 616 ILPQTPQGVVSLSRDLGEGSSSQD-----AGSCRPLHTDGSASPPMPDPSG 666  
 QY 343 YDSSVPSSELSLPLWEGSLTQETSSLTSSVSSSGSGEPEPPALPKLLSSGSC-CKA 401  
 DB 667 YDSSVPSSELSLPLWEGSLTQETSSLTSSVSSSGSGEPEPPALPKLLSSGSC-CKA 726  
 QY 402 DL 403  
 DB 727 DL 728  
 RESULT 4  
 Q8QEZ6 PRELIMINARY; PRT; 745 AA.  
 ID Q8QEZ6  
 AC Q8QEZ6  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)



Best Local Similarity 28.9%; Pred. No. 0.24; Mismatches 25; Indels 25; Gaps 8;  
Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 265 LVLDVNC-----KPGPESDFLKVEAVLGATGPDASQSHSGHGLDODGEARPAL 316  
Db 169 LGADLVCSLRMRERPGPTSPSIRKQ-----GASGAEGRRTDEEGREEG--APAP 243  
QY 317 DGSAAQLPILHTVVRAGSPDMDPSGIYDSSVP---SSELSPLMGLSTDTOTSSLTE 373  
Db 244 PGARA-----GGEGAGSPRTSRVSG--HTKIPDESEVTSSASEKILGR-QPRGRPHRE 295  
QY 374 SVSSSGILG-EEEPALPSKILSSGCKA 401  
Db 296 AADPRGSGSEEPASAPSLAAPSCSS 324

## RESULT 7

Q96KN9 ID Q96KN9 PRELIMINARY; PRT: 370 AA.  
AC Q96KN9  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Connexin40.1.  
GN CX40.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Eberberger J., Soehl G., Willecke K.;  
RT "Structural and functional diversity of connexin genes in the mouse  
and human genome."  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ1414564; CAC93846.1;  
DR InterPro: IPR000500; Connexin.  
DR Pfam: PF00029; Connexin; 1.  
DR PROSITE: PS00407; CONNEXINS.1; UNKNOWN\_1.  
DR PROSITE: PS00408; CONNEXINS.2; UNKNOWN\_1.  
SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;

Query Match 5.0%; Score 111.5; DB 4; Length 370;  
Best Local Similarity 28.9%; Pred. No. 0.26; Mismatches 25; Indels 25; Gaps 8;  
Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 265 LVLDVNC-----KPGPESDFLKVEAVLGATGPDASQSHSGHGLDODGEARPAL 316  
Db 211 LGADLVCSLRMRERPGPTSPSIRKQ-----GASGAEGRRTDEEGREEG--APAP 265  
QY 317 DGSAAQLPILHTVVRAGSPDMDPSGIYDSSVP---SSELSPLMGLSTDTOTSSLTE 373  
Db 266 PGARA-----GGEGAGSPRTSRVSG--HTKIPDESEVTSSASEKILGR-QPRGRPHRE 317  
QY 374 SVSSSGILG-EEEPALPSKILSSGCKA 401  
Db 318 AADPRGSGSEEPASAPSLAAPSCSS 346

## RESULT 8

Q9NT06 ID Q9NT06 PRELIMINARY; PRT: 428 AA.  
AC Q9NT06  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Hypothetical 45.4 kDa protein.  
GN DKF2434P211.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

SEQUENCE FROM N.A.  
RC TISSUE=TESTIS.  
RX MEDLINE=21154917; PubMed=11230166;  
RA Wiemann S., Neill B., Wellenreuther R., Gassenhuber J., Glassl S.,  
RA Ausorge W., Duescherboett A., Beyer A., Koehler K., Strack N.,  
RA Lauber J., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
RA Mewes H.W., Korn B., Klein M., Poustka A.;  
RA Wambutt R., Korn B., Klein M., Poustka A.;  
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and  
Analysis of 500 Novel Complete Protein Coding Human cDNAs."  
RL Genome Res. 11:422-435(2001).  
RL EMBL: AL117401; CAB55902.2;  
KW Hypothetical protein.  
SQ SEQUENCE 428 AA; 45443 MW; FA75BAC1A3FD83EE CRC64;

Query Match 5.0%; Score 110; DB 4; Length 428;  
Best Local Similarity 23.5%; Pred. No. 0.42;  
Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 139 KLRQAKQSS-SAALSKFIATVYDSCGDVPGI-----IDLSTKYRLMDNLQ 185  
Db 103 RYNQTSQTSWTSCTNRNAISSYSTGGLPARRGSPASSHCOLTUSSTKTVSDRQ 162  
QY 186 LCHLSHSDHGLQE--PGQHTGSGRRNYFRSGSLVAVICNMHOFIDEEPWFQK 243  
Db 163 AVSSGHTQCEKAADIAPGQTLT--LRNDSSTSEASRP-----STHKF---PLLPRRG 210  
QY 244 VFFH-PPPL-----RYRPFVLEKEDSLVINDVM---CKPGPSDFCLKVEAA 287  
Db 211 EPLMLPPLEGLGYVTVEDLDREKAAFORINSALQVEDKALSDCRSPRSH---TLSSL 267  
QY 288 VLGATG-PADSOHESGGLDGDGEARPDGSAALQPLHTVVRAGSPDMP-----RD 340  
Db 268 ATGASGLPAVSKAPS-----MDAQQETHSQDCLGLDPLASA--AGVTPAPSGKKHRP 321  
QY 341 SG-IVDSSVPSSELSPLMEGLSTDTOTSSLSVSSSGSLGEEPPALPSKILSSG 397  
Db 322 PGLPSSSDP-----LPATSSQDSQAQVTSLI-----PAPFAASMDAG 361

## RESULT 9

Q9AY10 ID Q9AY10 PRELIMINARY; PRT: 1058 AA.  
AC Q9AY10  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Putative gag-pol polyprotein.  
GN OSJNBA0087H07.4  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Pharbitidaceae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,  
RA Kim H.-R., Rambo T., Henry D., Simmons J.;  
RT "Rice Genomic Sequence."  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AC074283; AAK02020.2;  
KW Polyprotein.  
SQ SEQUENCE 1058 AA; 115228 MW; 9E39B2C564FC6CE7 CRC64;

Query Match 4.9%; Score 108; DB 10; Length 1058;  
Best Local Similarity 22.1%; Pred. No. 2.2; Mismatches 131; Indels 116; Gaps 21;  
Matches 85; Conservative 52; Mismatches 131; Indels 116; Gaps 21;

QY 116 HGGGGRSGKGLFLVAVSAIAEKL-----ROAKQSSSAALSKFIATV-- 157  
Db 204 NRGSGSGRGRDGRPKPTQCLGKRGVGTAKVCKWKFRDPSFTREKKSANTATSSSIDGT 263  
QY 158 --YFDYSCGDVPGILD-LSTRYRLMDNLQCLSHLSRHDHGLQEPCHTQGSRRNY-- 212

Db 264 NYVDSNATHITGEMKLSVDKYHGS-----EQVHAGCTGHEDANPARQNLRYNH 318  
 QY 213 -----PRSGSGSLYVAICNHO-----FIDEPDFEKFQVFP---HP-PPLR 252  
 Db 319 RLEFRSK-CAFLGISTHGFKCLIDISTGRVILSDV-VFDEQIYFANLHPNAGAR 375  
 QY 253 TREPVY-----BKFD-SGLVNDVMCKPG-----ESDFCLAYE 285  
 Db 376 LASEVLPLPDLPPYFOGGAIVNDOPMIDPNHTNQTAETDADRGAIVONSEPTGENN 435  
 QY 286 AVALGATGP-----ADSOHQHGLDQGEARPALDGAALQPLLTVAAG-----332  
 Db 436 ASNGCTEPGCHDFMGITSGGQHTGHPEDDAAASDASVA-----ESGNDGT 487  
 QY 333 SPEDMPDSG-IYDSVSPSLSLPLMEGLSTDTOTETSSLTSSVSSGL-----GREPP 387  
 Db 488 SPGACPTAAGHAESGOESSISAP-----HDSFASSTPGSDASSGVAESGGOQOP 540  
 QY 388 AL-PSKLLSSGCKADLCGRSYTD 410  
 Db 541 MLGPATSRGHIKP-----KRYTD 560

RESULT 10

Q88737 ID Q88737 PRELIMINARY; PRT; 3942 AA.  
 AC Q88737;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Bassoon.  
 GN BSN OR BASSOON.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129 SWJ;  
 RA MEDLINE-98345363; PubMed-9679147;  
 RA Dieck S., Sammarti-Villa L., Langnaese K., Richter K., Kindler S.,  
 RA Soyke A., Weh H., Smalla K.H., Kampf U., Franzer J.T., Stumm M.,  
 RA Garner C.C., Gundelfinger E.D.,  
 RT "Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively  
 RT localized at the active zone of presynaptic nerve terminals.",  
 RL J. Cell Biol. 142:499-509(1998).  
 DR EMBL: Y17034; CAA76598.1;  
 DR EMBL: Y17035; CAA76598.1; JOINED.  
 DR EMBL: Y17036; CAA76598.1; JOINED.  
 DR EMBL: Y17037; CAA76598.1; JOINED.  
 DR EMBL: Y17038; CAA76598.1; JOINED.  
 DR MGI:127955; Bsn.  
 SQ SEQUENCE 3942 AA; 418739 MW; 150267E36364DABC CRC64;

Query Match 4.9%; Score 107.5; DB 11; Length 3942;  
 Best Local Similarity 19.1%; Pred. No. 15;  
 Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;  
 QY 181 DNLPLQSLHLSRDHLOPFGHTRGSGRNTFRSGSLYVAIC-----NNHQFIDEE 235  
 Db 3535 DTCPQFCS-----SHSNPDQVBEHVDGPRAHAYKREGVYLDSDHCYVSDSEAYHLGQEE 3589  
 QY 236 PDMFKQVFPFPPPPRYRE-----PVLEKF-----DSGLVNDVMCKPG 275  
 Db 3590 TMDYK---PRDARSDFRHHGGHTVSSQKRGPARSHYDYDEPPEGLNPDH---EGG 3643  
 QY 276 PESDFCLVKAANVLGATGPADSOHQHSG-----GLDQDQ-----EAPP- 314  
 Db 3644 PQRE-----TSAREHHRHSDGHRHSGRHAGEPGRRAAKPHARDMGRRHARP 3691  
 QY 315 -----ALDGSAAALQPLHTV 329

Db 3692 PQASPAPAKQKQPCQIPSSADYSQSSRAPSAVHASBKSGKQRAHTGPSALQPKADTQ 3751  
 QY 330 KAGSPDMPRDSITDSSVPSSELSLEMLGLSTDTOTETSSLTSSVSSSGLGEZEPAL 389  
 Db 3752 APOKQGRQAAPGQSQPPSSRGT---PSGTASKQPTVQOQOQOQOQOQOQOQOQOQ 3808  
 QY 390 PSK 392  
 Db 3809 PSQ 3811  
 RESULT 11  
 Q902P6 ID Q902P6 PRELIMINARY; PRT; 1322 AA.  
 AC Q902P6;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Neuronal IL-16.  
 GN IL16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kirschner C., Yuzaki M.;  
 RT "Neuronal interleukin-16 (NIL-16): a dual function PDZ domain  
 RL protein.",  
 RL J. Neurosci. 19:0-0(1999).  
 DR EMBL: AF175292; AAD55393.1;  
 DR HSSP: Q14005; I1116.  
 DR MGI:1270855; I1116.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ; 4.  
 DR SMART: SM00228; PDZ; 4.  
 DR PROSITE: PS0106; PDZ; 4.  
 SQ SEQUENCE 1322 AA; 141434 MW; DDB94003ASDCB738 CRC64;

Query Match 4.8%; Score 107; DB 11; Length 1322;  
 Best Local Similarity 22.5%; Pred. No. 3.6;  
 Matches 71; Conservative 29; Mismatches 117; Indels 98; Gaps 13;  
 QY 138 EKLRQAQSSAALSFIATVFDYSCGDPVGLDLSKYRLMDNLPLQCSHL-----190  
 Db 282 QKFOAKK-----GLLTIVKRL-TTPPSLCSHLSPLCSRS 317  
 QY 191 -----ESRDBGLQEPQHTROGSRNT-----PRSKGSLYVAICNMHOFIDE 234  
 Db 318 LSSSTCGAQQDSSPFSLESPAS-PASTAKPNTRIMVETSLAKEAGVGLGICSLPYP---373  
 QY 235 EPDWEFKQVFPFPP-----PLRYEPVLEKFDG---LVLDVY-----CKPGP---276  
 Db 374 --QCISGIFVHTLSPGSAVHLGRLRCGDEIVINDSPVHCITLNEVITLSECDGPPV 431  
 QY 277 -----ESDFCLVKAANVLGATGPADSOHQHSG-----GLDQDQGEARPALDGAAL 322  
 Db 432 IIVSRHPDPQVSBQQLKNAQAQAVEGVKFGKDRHQSLEGVKRLSSWHEGRPTLEKERE-490  
 QY 323 QPLLHTVKAQSPDMPRDSIYDSVPSSELS-----LPLMEGLSTDTOTETSSLTSSVSS 377  
 Db 491 -----KHSAPPERRAOKIMVRSDDSYNSGSPGSPGSAQAEPQPSEREGSTHSPSL 543  
 QY 378 SSGLEGEPEPALPK 392  
 Db 544 SPGEQEPQCPGVSR 558  
 RESULT 12  
 O13399 ID O13399 PRELIMINARY; PRT; 757 AA.  
 AC O13399;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)

01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE Telomere-associated recQ-like helicase (Fragment).  
 GN UTASRECO.  
 OS Ustilago maydis (Smut fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
 CC Ustilaginaceae; Ustilaginales; Ustilaginaceae; Ustilago.  
 CN NCBI\_TaxID=5270;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=FB2;  
 RC Sanchez-Alonso P., Guzman P.;  
 RT "Organization of chromosome ends in Ustilago maydis: recQ-like  
 RT helicase motifs at telomeric regions."  
 RL Genetics 0:0-0(1998).  
 DR EMBL; AF030885; AAB95264.1;  
 DR InterPro; IPR001410; DEAD.  
 DR Pfam; PF00270; DEAD; 1.  
 DR SMART; SM00490; HELICASE\_C; 1.  
 KW ATP-binding; Helicase.  
 FT NON\_TER  
 SQ SEQUENCE 757 AA; 84382 MW; 1AE1E414435382A7 CRC64;  
 Query Match 4.8%; Score 105; DB 3; Length 757;  
 Best Local Similarity 20.6%; Pred. No. 2.5;  
 Matches 92; Conservative 42; Mismatches 147; Indels 166; Gaps 23;  
 QY 11 HLDSESSSTTAALP-----RERLRPRKVF-----LCYSSKDGQNMNVVO 54  
 DB 169 HVRDVTOTVMTATLPEDAFISHNKLKPLIVRESTNSNLCYVTAERASGMT 228  
 QY 55 CF-AVFLDDFCGCEVALDWDPSLCREGREWIKIHESOFIIVWCSKGMKVFVK-- 111  
 DB 229 CYDAVRVD--ECRARTDW-----NGQD-----RIIVYCT8--KELVARIA 267  
 QY 112 -----KNKHKGGGRG-----CGELELYAVSAIAKLRQAKQSSALSKFTA 156  
 DB 268 EMGCAANSSSEGEADKAATQDWICGSPVIVATSA-----LG 308  
 QY 157 VFDSCGDPVGL--DLSTY-----RLMDNLPOLCSLHLS 192  
 DB 309 VGDTPHVRVTHLGGDLLTDFSGRAGRGHFAEILLAGLDLDRAP--ASGKASS 367  
 QY 193 RBGLQEPQHTRGSRNNYFHSKGRSLYVAICNMHOFIDEEDPWFVKQVFPFPPPLR 252  
 DB 368 AEKGVAFG---ADKEAMQLYRSK---YCLRGVLSQLDQSDW-----406  
 QY 253 YREPVLEKFDGLVNDVMCKGPESDFCLVEAALVATGATGADSOH---ESQGGGLDQ 309  
 DB 407 -----RWCMEGDOLCSVCPGHHF-----QARGFGQGFHTAPAGQDPSTQ 447  
 QY 310 GEARPALGSAALPILFTVTKAGSDNPRDSGIYDSSVPSSE--LSUPLMEGLSTQTYT 368  
 DB 448 GSHPSMGSS--RPSMH-----GSSHPSSGSHSPSHSGSHPSIHG 488  
 QY 369 SLITSEVSSS---SGLGEERPALPSK 392  
 DB 489 SS-HPSIHSGQGGQRRRQQDPPE 514

## RESULT 13

Q24573 Q24573 PRELIMINARY; PRT; 901 AA.  
 AC Q24573;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE DEAD RINGER.  
 GN RTN OR DEAD RINGER OR CG5403.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidae; Drosophilidae; Drosophila.  
 CN NCBI\_TaxID=7227;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96182081; PubMed=8622680;  
 RC Gregory S.L., Kortschak R.D., Kalloniis B., Saint R.;  
 RT "Characterization of the dead ringer gene identifies a novel, highly  
 RT conserved family of sequence-specific DNA-binding proteins."  
 RL Mol. Cell. Biol. 16:792-799(1996).  
 DR EMBL; U62542; AAB05771.1;  
 DR TRANSFAC; T04679;  
 DR FlyBase; FBgn0004795; reln.  
 DR InterPro; IPR001606; ARID.  
 DR Pfam; PF01388; ARID; 1.  
 DR SMART; SM00501; BRIGHT; 1.  
 SQ SEQUENCE 901 AA; 96018 MW; 77200EC3601F7B8E CRC64;

Query Match 4.8%; Score 105; DB 5; Length 901;

Best Local Similarity 20.4%; Pred. No. 3.2; Matches 96; Conservative 56; Mismatches 157; Indels 162; Gaps 23;

QY 70 LDLWEDFSL--CREG-----QREW--VIQIHESOFI----IVVCSKGMKVF--VDR 111  
 DB 313 LDLYELYNLVIARGGLVDVINKLQWELIINGLHLPSSITSAFTLRQYMKLYPYCECK 372  
 QY 112 KNTK-----HKGGRSGSGKE-----LFLVAV 133  
 DB 373 KNLSTPAELQAADGNRREGRESSYQYEAHNMNPMPTISRPLPGGMQMSPLALVTH 432  
 QY 134 SAIAEKLR-QAKQSSAALSKEIATVFDYCEGDPGILDLSTKYLMNLPOLC----- 187  
 DB 433 AVANNQQAQAAAAAAAHRLMGA---PAFQGNLWVKQIESRMVEYL-QLIOAKE 487  
 QY 188 -----SHLESDBHGLQEPQH-----TROGRANTFRSKGR-----SL 221  
 DB 488 QGMPVTVGNGPEHQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQH 547  
 QY 222 TVAIACMHQ-----FIDEEDPWFVKQVFPFPPPL-----RYREPVLEKFD-- 262  
 DB 548 QVALMHTMHNNSPPGSAHNSPQQRREALNLSDSPNLTKREREREPTPEVDQDDKVF 607  
 QY 263 -----SGVLNDVMCKGPESDFCLAVE--AAVLGATGADSOHESQGGGLDQ 310  
 DB 608 DQPPAKRVGSGLL-----PGFPANFILNPMNMAAATAAG---FHPFSMGHQDAAS 658  
 QY 311 EARPALGSAALPILFTVTKAGSDNPRDSGIYDSSVPSSESLTPEG----- 360  
 DB 659 EGEPEDD-----YAHGEHNTGNSSMHDDSEPPQ-----MNGHHEHHTHLD 701  
 QY 361 LSTQTEFTSSITSEVSSSGLGEERPALPSKLLSSGCKADLGRSTYDE 411  
 DB 702 KSDSAIENSFTTITGSGVGRHSVPSTK--KKGKAPSGSGKDLPT 750

## RESULT 14

O54978 O54978 PRELIMINARY; PRT; 1571 AA.  
 ID O54978;  
 AC O54978;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Zinc finger protein.  
 GN PEG3.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CN NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96154192; PubMed=8563758;  
 RC Kuroiwa Y., Kaneko-Ishino T., Kagitani F., Kohda T., Li L.L., Tada M.,  
 RA Suzuki R., Tokoyama M., Shirolshi T., Wakana S., Barton S.C.,





GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 27.7988 Seconds  
(without alignments)  
2604.041 Million cell updates/sec

Title: US-09-912-157-2  
Perfect score: 1013  
Sequence: 1 MAPVLQCSVFVFNACLMG.....CQALGCRSYTDELHAYPL 753

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR-73:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3005	74.9	564	T42695	hypothetical prote
2	170.5	4.2	846	T27282	hypothetical prote
3	126.5	3.2	718	T30113	hypothetical prote
4	117	2.9	757	T03081	telomere-associate
5	117	2.9	917	T04661	hypothetical prote
6	116.5	2.9	2946	T00867	hypothetical prote
7	115.5	2.9	901	T03781	transposase (08) /
8	115.5	2.9	938	I49071	protein kinase - m
9	115	2.9	998	S37627	protein-tyrosine k
10	110	2.7	535	T17212	hypothetical prote
11	110	2.7	592	T49239	vesicle transport
12	108.5	2.7	3788	T13960	beige protein homo
13	107.5	2.7	3942	T42730	lysosomal traffic
14	107	2.7	3788	T30851	protein F1504.27 [
15	106.5	2.7	638	D86477	Subtilase family p
16	106	2.6	1448	A12007	dead finger nuclea
17	105	2.6	901	TJ0693	zinc finger protei
18	105	2.6	1571	T14155	protein-tyrosine-p
19	104	2.6	1462	B36182	GTPase-activating
20	103.5	2.6	663	A39897	Argonaute (AGO1)-1
21	103.5	2.6	930	A84668	ABR protein 2 - hu
22	102	2.5	859	A49307	98K GTPase-activat
23	102	2.5	882	A47485	ABR protein 1 - hu
24	101.5	2.5	1639	T50119	probable sensory t
25	101.5	2.5	641	T05497	hypothetical prote
26	101	2.5	664	T51247	ABR2 protein limpo
27	101	2.5	1275	A38985	nucleotide exchang
28	101	2.5	938	T05533	hypothetical prote
29	100.5	2.5			

30	100.5	2.5	974	2	E59434	Rho GTPase activat
31	100.5	2.5	1007	2	T4643	hypothetical prote
32	99.5	2.5	657	2	E96949	serine/threonine p
33	99.5	2.5	794	2	S59069	z13 protein - mous
34	99.5	2.5	981	1	POWVG4	gag-abl polyprotei
35	99	2.5	341	2	H71716	190 kd antigen pre
36	99	2.5	783	2	A31491	sex-determining re
37	99	2.5	970	2	S63059	hypothetical prote
38	98.5	2.5	353	2	T33782	hypothetical prote
39	98.5	2.5	963	2	A02381	type 1 site-specif
40	98.5	2.5	993	2	I48653	mouse developmenta
41	98.5	2.5	1050	2	G86582	exodeoxyribonuclea
42	98.5	2.5	1050	2	H72041	exodeoxyribonuclea
43	98.5	2.5	1050	2	C81624	exodeoxyribonuclea
44	98	2.4	526	2	T16134	hypothetical prote
45	98	2.4	820	2	S33794	hypothetical prote

## ALIGNMENTS

### RESULT 1

T42695 hypothetical protein DKFZp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 sequence\_revision 11-Jan-2000 text\_change 11-Jan-2000

C:Accession: T42695

R:Biocheck: H.: Biocheck: M.: Brandt: P.: Mewes, H.W.: Gassenhuber, J.: Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: K22230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFZp434N1928

C:Genetics:

A:Note: DKFZp434N1928.1

Query Match 74.9%; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8%; Pred. No. 8.5e-234;

Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy	190	HPFFFTACDILLOPNTACFPKPRNLNISQSGSDVDFHAPNCFEFTLYRK	249
Db	1	HPFFFTACDILLOPNTACFPKPRNLNISQSGSDVDFHAPNCFEFTLYRK	60
Oy	250	LKHEGPFKRTCKDEOTETTSCLLQNVSPGDYIIELVDVTNTKVMYALAPVHSPWA	309
Db	61	LKHEGPFKRTCKDEOTETTSCLLQNVSPGDYIIELVDVTNTKVMYALAPVHSPWA	120
Oy	310	GPTRAVATVPLVWISAFATFTVACRKQENIYSHLOESESSTYTAALPRELRPR	369
Db	121	GPTRAVATVPLVWISAFATFTVACRKQENIYSHLOESESSTYTAALPRELRPR	180
Oy	370	PKVFLCYSSKQGNHNVWCFAFYLFQDFCGCEVALDWFDFSLCREGQEWVQIKHES	429
Db	181	PKVFLCYSSKQGNHNVWCFAFYLFQDFCGCEVALDWFDFSLCREGQEWVQIKHES	240
Oy	430	QFTIIVVCKGKMYFDKKNYKHGGGSGKGFELFVAVSAIAEKLRQAKSSAALSXP	489
Db	241	QFTIIVVCKGKMYFDKKNYKHGGGSGKGFELFVAVSAIAEKLRQAKSSAALSXP	300
Oy	490	IATYFDYSCGSDVPGIILDLSTKYRLNDLNPOLCSHLSRDHGLQEPFGQTSRRNYR	549
Db	301	IATYFDYSCGSDVPGIILDLSTKYRLNDLNPOLCSHLSRDHGLQEPFGQTSRRNYR	360
Oy	550	SKSGSLVAVACNNHQFDREPNFEPKQVFPFHPPLRYREPVLKFGSLVLDVNCVPR	609
Db	361	SKSGSLVAVACNNHQFDREPNFEPKQVFPFHPPLRYREPVLKFGSLVLDVNCVPR	420
Oy	610	GPESDCLKVAANVLGATGPASQSHSGGLDQDGEARPDGSGAALQPLHTVYKASP	669
Db			

Db 421 GPESDFCLKVAEAVLGTATGPAUSQHSQHGGLDQGEARPALDGAALQPLHTTVKAGSP 480  
 QY 670 SDMPRSGTYDSSVPSSLSLPLMGLSTDTOTETSSITVSSSGLGEEPPALPSKLL 729  
 Db 481 SDMPRSGTYDSSVPSSLSLPLMGLSTDTOTETSSITVSSSGLGEEPPALPSKLL 540  
 QY 730 SSGCKADLGGCRSTTDELHAPL 753  
 Db 541 SSGCKADLGGCRSTTDELHAPL 564

## RESULT 2

T27282

hypothetical protein Y64G10A.e - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000

C:Accession: T27282

R:Alnscough, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20336

A:Accession: T27282

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-846 &lt;NLS&gt;

A:Cross-references: EMBL:AL104048; PIDN: CAB54470.1; CESP: Y64G10A.e

A:Experimental source: clone Y64G10A

C:Genetics:

A:Gene: CESP:Y64G10A.e

A:Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3

C:Superfamily: Caenorhabditis elegans, hypothetical protein Y64G10A.e

Query Match 4.2%; Score 170.5; DB 2; Length 846;  
 Best Local Similarity 21.4%; Pred. No. 3.3e-05;  
 Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;

QY 99 QVACHDQVAVTILWSPGALGIEFLAGFVILELKGRCQCOLLIDKPOLANSSFRKG 158  
 Db 294 QY-CFEEFEVLLDSS--GIVMLASALITKDELRYE-----IINGRPQVFEP----- 338  
 QY 159 MESQPLNKKETDYFVKKVPPFSKINESNHHFFRTRACDLILLQPNLAC-KPWKKR 217  
 Db 339 ----NFTDIELDTLIPVIPIESAHD-----GRC-LCVTEGGSCLAADMKRV 382  
 QY 218 NINISQSGDQVSDFDHAPNFGFRFYLYHKLKHEGPPKRTCKQETTTSCILLNV 277  
 Db 383 KLT-----RIKKPATSN-----QTESDGAEKAKKEITWT----- 415  
 QY 278 SPGDYIIELVDVTNTTKVMH-YALKPVHSPWAGPIRAVAITVPLVVISAPATL--FTVM 334  
 Db 416 -----WHYTA-----ITGGAITAILFILSVCAGLAKYKEF 445  
 QY 335 CRKQKQENITSHLDESSSTTTAALPRELPRKPKVLCYSSKDGONHNVVQCFAYF 394  
 Db 446 NKKKASHI--HLLENPAFS-HSGSIFL-ILKQISLVITV-SDSQAHEAAVLAPAE 500  
 QY 395 LQDFCGCVALDWHEDFSLCRGQREWYQKHESQFIIVVCSKGMKTFYDKNKKHKG 454  
 Db 501 LKDVFNLAHVLDWDEDDI-EENRAEYINSIVRANKVIIINSIG-AYF--RTVFRHQ- 555  
 QY 455 GRSGKGGLFIVAVSAIAEKLQAKQSSAALSFKFIATVFDYSCGDV--GGILDLSKY 512  
 Db 556 -----EPAIERITTGND-----VIFDMOCELALQHPVICSHESY 591  
 QY 513 -----RLMD-NLPQLCSLHSDHGLQPGQHTROGSRNRYFRSKSGSLYVAI 560  
 Db 592 TNPKYVFPPINLLQYSIP--NSLWMTYFALTEQAPAEQLAGENQVFAR----LQAI 644  
 QY 561 CNMHQFIDEEDWFEK-----QFVDFPHPPPLRTH----- 589  
 Db 645 SRKLANIESDPQWENHHRVATRVKSELAHNIVPL-PPSLEYKVEDAFQOMETLPI 703  
 QY 590 EPVLEKF-----DSGLVNDVMCKPGPESDFCLKVAEAVLGTATGPAUSQHS 636

Db 704 DELKEKFAKREDLEVLDSEDDVKKLLEDVCAKCP-----LHVTEPEVLEPAEPMEE 758  
 QY 637 QHGGLDQGEARPALDGSNA-----LQPLL-HTVKAGSPDMRPGSGIYDSS-VPSSLS 689  
 Db 759 AEED-EEDEDDVDSVGGTARTEELQLNLIH-----KMHDSGMLDSATVSGSDFS 809

## RESULT 3

T30113

hypothetical protein F56D1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T30113

R:Chissos, S. Y. Wilson, R.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F56D1.

A:Reference number: Z20737

A:Accession: T30113

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-718 &lt;CHIT&gt;

A:Cross-references: EMBL:U39997; PIDN: AAA81100.1; CESP: F56D1.2

C:Genetics:

A:Gene: CESP:F56D1.2

A:Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3

C:Superfamily: Caenorhabditis elegans, hypothetical protein F56D1.2

Query Match 3.2%; Score 126.5; DB 2; Length 718;

Best Local Similarity 21.1%; Pred. No. 0.091;

Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;

QY 363 RERLRPRP-----KVFICYSSKDGONHNVVQCFAYFLQDFCGCFVALDWDIFS 412  
 Db 398 RDKVRSREVRNIALTEFYKVMIVAD-DNDLEFDCVKLVENLRNCASCPDFLEKLT 456  
 QY 413 LCRCQREWYQKHESQFIIVVCSKGMKTFYDKNKKHKGSGKSGELFVAVSAIA 472  
 Db 457 ABQIVPSRWLVQDISLKAFIIVSDCAEKILDTSEATHQIVQARRPADLPANEMI- 515  
 QY 473 EKLQAKQSSAALSFIATVFDYSCGDV---GILDLSKYRLMDNLPQLCSLHSDR 529  
 Db 516 ---IDATENTPEARKKIYAVVRNYS--PHYPPNIALAILNLT-FILPEQPAQLATLHVE 570  
 QY 530 HGLAPQGHTRQGRNRYFRSKSGRSY---VAICNMHQFIDEEDWFEKQVFP----- 580  
 Db 571 H-----TERANVTNITSEAIHNNLCASRWMSFFVRNPWLETRKKPKDELA 619  
 QY 581 PHPPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVAEAVLGTATGPAUSQHSQHG 640  
 Db 620 LH--LKRQSFVIVPIOT-----EED---RLAASIKYKLVPPQALVSD- 657  
 QY 641 LDQGEARPALDGSALQPLHTTVKAGSPDM--PDGSIYDSSVPSSLSLPLMEGLST 698  
 Db 658 -DED-----DVDLQF--HSHQNPQLILLPPEQCG-----PDSD-----SD 690  
 QY 699 QGTETSSLTSEVSSSSGLGEEPPALPSK 727  
 Db 691 SESDSSSESESDNEG--EDPKTIIVVK 716

## RESULT 4

T09081

telomere-associated reco-like helicase - smut fungus (Ustilago maydis) (fragment)

C:Species: Ustilago maydis (corn smut)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-May-2000

C:Accession: T09081

R:Sanchez-Alonso, P.; Guzman, P.

Genetics 148, 1043-1054, 1998

A:Title: Organization of chromosome ends in Ustilago maydis: reco-like helicase motif

A:Reference number: Z16557; MUID:98198830; PMID:9539423

A:Accession: T09081

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-757 <SAS>

A:Cross-references: EMBL:AF030885; NID:92642221; PID:92642222

A:Experimental source: strain FB2

C:Genetics:

C:Gene: OTASRECQ

C:Keywords: DNA binding

Query Match 2.9; Score 117; DB 2; Length 757;  
Best Local Similarity 20.4; Pred. No. 0.57;  
Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;

QY 268 ETICLLQNSPDYIIELVDVTVTRVNHVALPVSPWAGPIRAV---AIVPL-- 321

DB 77 ETTILILPTVALRANLAKLDVM---IRYHWOP-GSKAADIIVLYSTEARIVLAKKE 131

QY 322-----VLSAFATLFTVWCKKQENIYSHLDESSESTYTAAP----- 362

DB 132 YANRLQOOLRIVIDECHTLFARSTRSMQLANVRDVEVTVMLTATLPIDFA 191

QY 363---RERLRPRKVF-----LCYSSKDGQNHVYVQCF-AIFLDQPCGCEVALDMEF 411

DB 192 FISHKILKPLIVRESTNRLCYSTVTAHERMSGTCYDAVRVD--ECRARTDIW--- 246

QY 412 SLREGQREWVQIKHESQFIYVCSKGMKIFVDR-----KNYKHGGGRGS----- 458

DB 247-----NGORD-----RIIVYCTS--KELVARLAEMLCGAATSESGSEADKAAIIQ 290

QY 459---GRELPLVAVSAIAELKRAQKSSAALSKEFIATYFYSCGDVPCIL--DLSTKY 512

DB 291 DWICGKSPVIVATSA-----LVGVEDYPHVRVHLLGPOLLIDF 331

QY 513-----RLMONLPOLCSHLHSDHGLQEPQOQTRQGRNRTFRS 550

DB 332 SQESGRAGRCHPAREILLACQLDDRAP-ASGKASSAERGKVAQP---ADKEAMQLTRS 387

QY 551 KSGSLVLAICNNHOFIDEEPDPWEKQFVFPHPPLRYREPVLEKFDKSLVNDVACKPG 610

DB 388 RK-----TCLRGVLSOLLQDSDM-----RRCMEGDQLCSVC 419

QY 611 PESDFCLKVEAAVLGATPADSQR---ESQHGGLDQGEARPALDGSAAALPLLHTYKAG 667

DB 420 PGHFF-----QARGPGDQFHTAPAQAGDPSTQGRHPSMEGSS--HPSME----- 463

QY 668 SPSPMDRSDGIYDSSVSPSE--LSLPLMEGLSTDQETSTLSTESVSSSS--SLGGEERPPA 723

DB 464-----GSSHPSSHGSHPSHSGSHPSHSGSS--HPSHSGHGGQGRKQKQPD 510

QY 724 LPSK 727

DB 511 PPSE 514

RESULT 5

T04661

hypothetical protein F8D20.70 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 24-Nov-1999

C:Accession: T04661

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Meves,

submitted to the Protein Sequence Database, July 1998

A:Reference number: Z15381

A:Molecule type: DNA

A:Accession: T04661

A:Residues: 1-917 <BEV>

A:Cross-references: EMBL:AL031135

A:Experimental source: cultivar Columbia; BAC clone F8D20

C:Genetics:

A:Map position: 4

A:Introns: 13/3; 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3; 685

A:Note: F8D20.70

C:Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70

Query Match 2.9; Score 117; DB 2; Length 917;

Best Local Similarity 19.3; Pred. No. 0.76;  
Matches 167; Conservative 130; Mismatches 296; Indels 320; Gaps 42;

QY 19 NGSQLAAVAGGSGRARGADTCGRM--KAAARPR---LCVANEGV----- 58

DB 92 NGRSVS---GYSNG-DILWISIPSGKGCSPSSAMICKLNLGYKSEKIPASLAKWY 145

QY 59--GPASR-----NSGLNITFYDNTTYLNPVGKV---IADAONI--TISOTACHDQ 105

DB 146 AEGKASRVTVICSSNSLOVLLNEOTETRMKLGHSVSEPCADMEKILADVNEOSRHKQ 205

QY 106 VAVTILWSPCALGI---EFLAGFVILEELKSGROCOOLILEDKPOLNSSFATGMSOP 163

DB 206 DFLVFLGKGRVATDDTHIEKYLQSKSPSLPRTVVKLPFFSDSSITVYKGFITNP 265

QY 164--PLMKFFDY-----FVKVVPFPIKNSN---YHPFF-----FTRACOLLQPD 206

DB 266 SHLNLSDE-DYALAKDAVPLPFTVPKSSSAHPGPTKRVNVIYTGCDGTSVW 324

QY 207 NLACK-----PFWKPR-NLAISQBG-----SDQVSEFDHAPENFGFFFLHY 248

DB 325 DMTCSPILVLEKQIDODVSSRGNAALTALHYDSNRLVSGDNGVRLYRFPKPEY 384

QY 249 KLRH-----EGPKR-----KCKQEQTTTTCCLQNVSP-----GDVIELV 287

DB 385 LTENSFIPOGSLAKGNHIVQSVKIKLTGTSITCQKSONSKHLAIGSDGHSLEVI 444

QY 288-DDTNTTRKVMYAKPVHSPWAGPIRAVAITVPLVVISAPATLFT----- 332

DB 445 D-----ALPPT-----LQVSLVDEEANVLYTKHISDLCIGLISLQ 482

QY 333-----VMCKKQENIYSHLDESSESTYTAALPRERLRPRKPVLYCYSSKD 380

DB 483 FESCIVOGFEKVLVAVMARDSSVFA-LDSDTGNMIGTNNMKPR-----KPFVLYTMOILD 536

QY 381 GQHNHVQCFATFLQDPCGCEVALDLDWEDFSLCREGOREWVQIKHESQFIYVCS-- 437

DB 537 GK-----QDTSQ-----NGFDTRES-----TVEEISIRQPSVLVCSKA 571

QY 438-----KGMKYVDKKNYKHKG-----GGRGSGKGEFLVAVSAIAE---K 474

DB 572 IYVLSLARVQGVKVLKHKFSSPICSSASTFTGTSGV---LTIVFTDGTVEIRSLPE 628

QY 475 LRQAKS-----SSAALKEFANFYDYSCGD-----VPGILDSIKYRLMD 516

DB 629 LSQKQTSIRGFTSSPKNSLPEITISASNDGDLVWVNGDDELVSUPLDQKETERIVE 688

QY 517 NLPOLCSHLHSDHGLQEPQOQTRQGRS-----NTRFSKSGRSUTYVAICNMHQFIDEE 570

DB 689 SH-----NRVYKDNISVCHGIIITSSSPKSKMFGSVFKTKSKRTTIDTEPSSKETEEL 744

QY 571 PMWFKQFVFP-----HPPLRYEPVLEKFD 598

DB 745 SKIFSTANFPMNNVNSREINTITVEDEELDIDDDHHPNOQOQKPEQIGLS 804

QY 599 GL-----VLADVMCKRPGSPDFCLKVAEAVLGATGADPSQESOHGGL----- 641

DB 805 GLSKQKMANFSEFKGLKQAKNEKSVV-----TNDKEHEENGATVDOIKKKYGTSS 860

QY 642 DQDGEARPALDSAAQLPPLLHTYKAGSPDMRPGIYDSSVPSSELSPLMEGLSTQOT 701

DB 861 DEMGAANA-----QSKLD-----NLKQLQGISLRTT 888

QY 702 ETSLSLTFESVSSSS 714

DB 889 EMEETAKSFSSTA 901

RESULT 6

T00867

hypothetical protein At2g45540 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F17K2.7

C:Species: Arabidopsis thaliana (mouse-ear cress)

QY 486 -LSKFIANYTDYSCBQDVGILDLSTKYRLMDL--PQLCSHLHSRDLQOE-----PQGH 538  
 Db 897 DLRLLLGFIIDSPQPNQVNRVLHLMYRLVQPNNAARQAQFAEVFTTSGCIETLLVLLQRE 956  
 QY 539 TRQSRNRNYFRSKSGSLSTVAICNMHOFIDEEDPWEKQFVFPHPLRYREPVLEKFDG 598  
 Db 957 ARTGEDNVLAMGRSGRR-----SSTDPSSEK--PYN-----ESGSVRLQDGS 995  
 QY 599 GLVLDNV-MCKPQPSDEDFCLKYEAALVGGYG-PADSCQHSQRGGIDGDEARPALDGSAA 656  
 Db 996 NPHDNEIGFDLPQPDGN--SVEEDNVGSLNVLPESVROKKEG-----1035  
 QY 657 LQPLHVTYKAGSPDMRDSGTIYDSSVPSELSLPLWEGSLTDOTETSSILTESVSSSGL 716  
 Db 1036 -----STWVCDSVSVISNINTEKLS-----AEIGGISLSIDSASR 1074  
 QY 717 GE---EEPPA-----LPSKLLSSGSCADLGCRS 742  
 Db 1075 NNVTNVDSNVVVGIIIRLIGALISSGHLTFDFDQARS 1111

RESULT 7  
 F83781  
 transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported]  
 C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000  
 C:Accession: F83781  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, P.;

A: Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans*  
 A: Reference number: AB3650; MUID: 20512582; PMID: 11058132  
 A: Accession: F83781  
 A: Status: preliminary  
 A: Molecule type: DNA  
 A: Residues: 1-901 <GTO>  
 A: Cross-references: GB:AP001510; GB:BA000004; NID: g10173440; PIDN: BAB04773.1; GSPDB: 8  
 A: Experimental source: strain C-125  
 A: Genetics:  
 A: Gene: BH1054

Query Match 2.9%; Score 116.5; DB 2; Length 901;  
 Best Local Similarity 19.6%; Pred. No. 0.82;  
 Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY	61	ASRSGLYNIITFYDNCITYLNPVKVIADAQNITISQY-ACHDQAVATILMSPCALGI	119
DB	333	ALKESSL	371
QY	120	EFLKGFVILEELKSSGR-----QCOOL--ILKDPQLNSPFKFGMESOFFLIMKPF	169
DB	372	---HTFR--QEQRSFAKRRHPYNWICDETDVYCPNQRKVSFKYTKRTDTPY---GY	423
QY	170	ETDIFV-----KVPFP-PSI-----KNEYNIPFFPFRTRACDILLOPNLACKPFWKPR	217
DB	424	ARDKVFYECESGCGFPKPECTKARGNQVHYNPVT-----EELKAKQKQKLK	471
QY	218	NLNTSQHG-----SDMQVSPDHPAHPNGFPFFLYHLKLBHEGPFKRYTCQEQTTET	269
DB	472	---SEGRTLIQKRKTIDVESFGHVKNIGFARLLRCK-----	507
QY	270	TSCLLQNVSPCDYIIELVDVDTNTTKVMHYALKAPVHSPWAGPIRAVAITVPLVVIS-AFA	328
DB	508	-----ESVHIELGLVALAHLNR	524
QY	329	TLFTVMCKKKGNIYSHLDRESSESSTYTAALPRRLAPRPKVPCLCVSSKQGNHNVV	388
DB	525	KNAVDRSRKPAHTMOKHNEN-----RIKRF-----SRFYVL	558
QY	389	QCF---AYFLQDFCGEVALDWEDFSICRQGEWV---TQKIHESQFTIYVVCSGMK	441
DB	559	RCFWDSPFFIKDGKQYASFALEF--KLRRGEGENMIEVLDLSKTYRNRQV---KGIN	612

Query Match	2.98;	Score 116.5;	DB 2;	Length 901;
Best Local Similarity	19.6%;	Pred. No. 0.82;		
Matches 112;	Conservative	76;	Mismatches 169;	
Gaps 27;			Indels 215;	

Db 613 MFIEKGVLLGPNAGKSTTSMISSIQPTSGDVLKIGSGSIHQSKATIESILGVVQ 672  
QY 489 FIAYFYDICE-----GDVFGILDSTYRLMQLPQACSHLSHSDHGLQPGQRTROG 542  
Db 673 EIAVTHDIARENAFFKTYIGLGBELAKR-NESTLQV-----GLEE-----RON 718  
QY 543 SRMYFRSKSGSLVAICNMHQ---FIDEER 571  
Db 719 DRVTFSGGKRLNIAVALLHPELLINDER 750

## RESULT 8

149071

Protein kinase - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999

C:Accession: I49071

R:Kuliz, J.C.; Conlon, F.L.; Robertson, E.J.

Mech. Dev. 48, 153-164, 1994

A:Title: Identification of novel protein kinases expressed in the myocardium of the deve

A:Reference number: 149071; MUID:95200798; PMID:7893599

A:Accession: I49071

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-938 &lt;RES&gt;

A:Cross-references: EMBL:U11493; NID:q595418; PIDN:AAA67925.1; PID:q595419

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat

C:Keywords: ATP; transmembrane protein

F:571-839/Domain: protein kinase homology &lt;KIN&gt;

F:579-597/Region: protein kinase ATP-binding motif

F:1864-938/Domain: SAM homology &lt;SAM&gt;

Query Match 2.94; Score 115.5; DB 2; Length 938;

Best Local Similarity 19.44; Pred. No. 1;

Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;

QY 9 SVFTFVNAQL-NGSLAVA-----AGGSQR---ARGADTCGRMKAAARPLC-----52

Db 170 SLVTAPRACIANAVSVPLKLYCNGDGEWVPVGCATCATGHEPAKESQCRACPGSY 229

QY 53 VANEGVGPA-----SRNSG-----LYNIFKYDN-----CTYLPVGVKRVIAQAQ 93

Db 230 KAKGEGPCPLCPNPSRTTSPASICTCHNFFRADSDSADCTTRSP-PRGVISNV- 287

QY 94 NITISQYACHDOVAVTILMS-PCALGIEFLAGFRVILEELK-SEG-----RCCQLIL 144

Db 288 -----NETSILLENSEPRDLGRDDLLYNVICKKCGSGGAGGATCSCRDDNVE 337

QY 145 KDPQLNSFKTKTGESOPFLNKKFTDYFVVPFPIKNSNYHFFFRACDILLQ 204

Db 338 FVPQLGLTERVHVS-----HLLAHTRTFEVQAVNGVSGKSLPPLRYAAVNTTQAA 392

QY 205 PDNLACKPFWKPRNLNLSQSGSDQVSDPHAPNFGFRFYLYKLBHGGP-RRKTCQ 263

Db 393 PSEY-----PTLHSHSTGSSLTLSWAPPENPNG---VILDYENKY---PEKSKAIA 439

QY 264 EQTTETTSCLLQNVSP-GDYIELVDVDTNTRKV-----MHALKPVHSPWAGPIRAVA 316

Db 440 TVTSQKNSVOLGLQPDARTYVQV-----RARTVAGYQYTHPAEFETTSERGSQAQLQ 494

QY 317 ITPLVVISAPA-----TLFVVCRRKQKENIYSHLOESESSTTAAALPRRLRP 368

Db 495 EQPLVGVNAGVFWVWVVAALVCLRKQRH-----GPDARTYTEL-QQYIAP 543

QY 369 RPRVFLCYSKDQGNMNVQCFAYFLQDFC-GCEVALDWEFSLCREGQEWYIOKIH 427

Db 544 GKNYIDPTTYEDPN--EAVREFAKEIDVSCVKEIEVIGAGEGECV-----589

QY 428 ESQFIIVCSKGMFYVDKKNYHKGSGSGKGLPLVAVSAI-----AKLRQAKOSS 483

Db 590 -----GELKLPGRREVF-VAIKLVGYTTERDRFLSEA 623

QY 484 AALSKFIAYFIDISCGDVFGILDLS-----TKYR-----LMDNLPQACSHLSHSDHGLQ 533  
Db 624 SRNGQP-----DHNFIIRLEGVVTKSRPVMTLTFEENC-ALDSFLRLND-----667  
QY 534 EPQCHT-----RQSSRRNT-FRKSQSGSLVY---AIC-----NHQFIDE 569  
Db 668 --GOFTVQLVGLKRGIAAGKYLSEMTVHRDLAARNILVNSNLVCKVDFGLSRELD 725  
QY 570 EPDWEKQP-----VPEH---PPPLRYREPLEKFDG-----GLVLDNVCKGPE 612  
Db 726 DPS--DPTYSISLGGKIPRWTAPEIATR-----KDSASDVNSVIGVMEVMS-----773  
QY 613 SDFCLVAEAVLGTGADPADSQHSGHGLDQGEARPALDQSAALQPLHIVKAGSPDM 672  
Db 774 -----YGEPTWNSNODDINAVEQDYLPPPMOCPTALHOLMASCWYDRNLR 822  
QY 673 PROGGIYD-----SSVPSSELSLPLMEGLSTDOT 701  
Db 823 PKFSQIVNTLDKLIRNAASLKVTSAPSG-MSQPLLDRTVPDYT 865

## RESULT 9

S37627

protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human

C:Species: Homo sapiens (man)

C&gt;Date: 19-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 04-Feb-2000

C:Accession: S37627

R:Boehme, B.; Holtzsch, U.; Wolf, G.; Lutz, H.; Grzeschik, K.H.; Strebbardt, K.; Ru

Oncogene 8, 2857-2862, 1993

A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.

A:Reference number: S37627; MUID:93390963; PMID:8397371

A:Accession: S37627

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-998 &lt;BO&gt;

A:Cross-references: EMBL:X5208; NID:q406867; PIDN:CAA53021.1; PID:q406868

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea

C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein

F:631-899/Domain: protein kinase homology &lt;KIN&gt;

F:639-647/Region: protein kinase ATP-binding motif

F:922-988/Domain: SAM homology &lt;SAM&gt;

Query Match 2.94; Score 115; DB 2; Length 998;

Best Local Similarity 19.04; Pred. No. 1.3;

Matches 158; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

QY 35 GADTCGRMKAAARPLC-----VANEGVGPA-----SRNSG-----LYNIFK 73

Db 267 GACTCATGHEPAKESQCRPCPGSTKAKGEGCLPCPNPSRTTSPASICTCHNFR 326

QY 74 YDN-----CTYLPVGVKRVIAQAQNTISQYACHDOVAVTILMS-PCALGIEFLKGR 126

Db 327 ADSDSADSACTVPS-PRGVISNV-----NETSILLENSEPRDLGRDILLN 374

QY 127 VILEELKSG-----RCCQLILKDPQLNSFKTKTGESQPLNKKFTDYFVVPFPP 181

Db 375 VICKKCHGAGGASACRCDNVEFVPRQLGLSEPRVHTS-----HLLAHTRTFEYQAVN 429

QY 182 SIKNESNYHFFFRACDILLQPDNLACKPFWKPRNLNLSQSGSDQVSDPHAPNFGP 241

Db 430 GVSGKSLPPLRYAAVNTTQAAPEV-----PTLHSHSTGSSLTLSWAPPENPNG- 481

QY 242 RFTLYLKLHGGPP-RRKTCQKQDTTETTSCLLQNVSP-GDYIELVDVDTNTRKVHY 299

Db 482 --VILDYENKY---PEKSEGIATSTVSQNSVQLDGLRDPARTYVQV-----RARTVAGY 531

QY 300 A--LKPVH---SPWAGPIRAVAITVPLVVISAPATL-----FTVMCRKQKENIYS 345

Db 532 GQYSRAPEFETTSERGSQAQLQEQPLVIGSATAGLVFVAVVVAIVCLRKQRH-----587

QY 346 HLBESSESSTTAAALPRRLRPFRPVFLCYSKDQGNMNVQCFAYFLQDFC-GCEVA 404

Db 588 -----GSDSEYTEKL-QQYIAPGKNYIDPTTYEDPN--EAVREFAKEIDVSCVKEIEV 638

QY 405 LDLDNEDFSLREGREWVQIKIHESOFIIVVCKGMYFVCKNKKHGGGSGKGLF 464  
Db 639 IGAGEGVECR-  
QY 465 LVAVSAI-----AKLQAKQSSAALSKEFIANTFYDSCEGVPGIILDS--TKYR-----513  
Db 662 -VAIKTAVGTQRRDRLSEASINGQF-----DHPMIIRLEGVTKSRPMI 709  
QY 514 ----LMDNLPOLCSHLASRDHGLQEPQHT-----RQSRNRY-FRSKSGR 554  
Db 710 LPEFMENC-ALDSFLRLND-----GOFTVQLVGNLRIAGAGMKYLSNNYVHRDLAAR 762  
QY 555 SLTV-----AIC-----NMHOFIDEPDFWFERQFVPHPP-----PLAYREP---VLEKFD 597  
Db 763 NMLVSNLVCKVSDFLSLFLEDOPS-----DPTTSSILGKIPIRWTAPEALAKFT 816  
QY 598 S-----GLVLDNVMCKKPGPESDFCLKVEAAVLGATGAPDSOHSOHSOGLDQDGEARPA 650  
Db 817 SASDVMSTGIVMEVMS-----YGERPYDMSHQDYINAVEQDYRLPPP 860  
QY 651 LDGSAALQPLHTVTKAGSPDPSGDIYS-----SVPSSELSLIMGL 696  
Db 861 MDCPTNLHQLDCWYDRNLKAPFSQVLTLDKLIRNASLVKVASQAGMSOPILORT 920  
QY 697 STDQFSTSTESVSSSSGLGEEPPALPSKLLSGSCADIGCRSTYDEL 747  
Db 921 VPDYTFITVGDWLDIAIK-MGRYK-----ESFVSAGFASFDVAQMTAEDL 965

RESULT 10  
T17212  
hypothetical protein DKF2p434P211.1 - human (fragments)  
C:Species: Homo sapiens (man)  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
R:Accession: T17212  
R:Pousta, A.; Kleio, M.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A:Reference number: Z18723  
A:Accession: T17212  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-488/489-535 <POD>  
A:Cross-references: EMBL:AL117401  
A:Experimental source: adult testis; clone DKF2p434P211  
A:Note: the cDNA sequence contains a -1 frameshift near codon 488  
C:Genetics:  
A:Note: DKF2p434P211.1

Query Match 2.78; Score 110; DB 2; Length 535;  
Best Local Similarity 23.5%; Pred. No. 1.3;  
Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;  
QY 474 KLRQAKQSS-SAALSKEFIANTFYDSCEGVPGI-----LDLSTKRLMDNLPQ 520  
Db 103 RYNQTSQTSMTSCTRNASSTSTGGLPKRRRGPASSHCQLTSSKTSVSDRQP 162  
QY 521 LCSHLASRDHGLQEPQHTROGSRNRYFRSKSGSLYVAICNMHOFIDEPDFWFERQF 578  
Db 163 AVSSGHTQCEKAADIAPGQTLT--LRNDSSTSEASRP-----STHKF----PLAPRERG 210  
QY 579 VPFH-PPPL-----RYREPVLKFDGLVLDNVM---CKPGPESDFCLKVEAA 622  
Db 211 EPLMLPPLLELGYVTVEDLDREKAAAFQINSALQVEDKAKISDCRPSRSH---TLSSL 267  
QY 623 VLGATG-PAUSOHSOHSOGLDQDGEARPAALQPLHTVTKAGSPDMP-----RD 675  
Db 268 ATGASGLPAYSKAPS-----MDAQETHKSQDCGLDPLASA--AGVSTAPMSKGRHP 321  
QY 676 SG-ITDSSVPSSELSLPIAMEGLSTDTQTETSLTESVSSSSGLGEEPPALPSKLLSG 732  
Db 322 PGLPSSSDP-----LPATSSDSQDSAQVTSLI-----PAPPPAASMDAG 361

RESULT 11  
I49239  
vesicle transport protein - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
R:Accession: I49239  
R:Tellam, J.T.; McIntosh, S.; James, D.E.  
J. Biol. Chem. 270, 5857-5863, 1995  
A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neur  
A:Reference number: I49238; MUID:95197608; PMID:7890715  
A:Accession: I49239  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-592 <RES>  
A:Cross-references: EMBL:U19521; NID:9642027; PIDN:AAA69913.1; PID:9642028  
C:Genetics:  
A:Gene: munc-18c

Query Match 2.78; Score 110; DB 2; Length 592;  
Best Local Similarity 18.5%; Pred. No. 1.5; Indels 188; Gaps 22;  
Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;  
QY 321 LVWISAFATLFTVCKKKQ-----ENIYSHLDESESESTYTAALPRERLRPRK 371  
Db 34 IMLDEFTTKLLSSCKMTDLLEGITVTIENYKKNREPVRQMKALYF-----ISPTPK 86  
QY 372 VFLCYSSKQGNHNVVQCFAYFLQDFC-----GCE-----402  
Db 87 SVQCFRLDFGSKSEKKYKAAVYITDPCPSLNFNIKASCSSKIRKKEINLSFIPQESQ 146  
QY 403 -VALDLWEDFSLC-----REGREWVQIKIHESOFIIVVCK-----SKMKY-----442  
Db 147 VTTLDVDAFTCYTSPDPSNARSREYVMEARQ--IVTVCATLDENPGVYKSKPLDNA 204  
QY 443 -----FVCKK---NKK--HGGGSGSGKGLFV-----AVSAIKLQAKQSSAALS 487  
Db 205 SKLAQLVERKLEEDYTRIDEKGLIKGTQSLLIIDRGDPVSVVLHEL-----252  
QY 488 KFIAYFD-----YSCG-DVPGIL-----DLSTKYR-----LMDNLPOLCSHL 536  
Db 253 TFQAWAYDLPLIENDYTKYDKGEKEAVLEEDDLVVRVNRHRIAVLLEIPKLMKEIS 312  
QY 527 SRDGLQEPQHTROGSRNRYFRSKSGSLYVAICNMHOFIDEPDFWFERQFVPPHPP 586  
Db 313 STK-----KATEKTSLSALTQLMKKMPFRKQISKQVV-----HL 348  
QY 587 RYREPVLKFP-----DSGLVLDNVMCKKPGPESDFCLKVE 620  
Db 349 NLAEDCNKFKLNIEKICKTEQDLALGTDAGQVKDSMLVLLPVLL--NKNHNDCKIR 406  
QY 621 NAVLGATGAPDSOHSOHSOGLDQDGEARPAALQPLHTVTKAGSPDMPRD-SGIY 679  
Db 407 AVLLTIIFGTINGTEEN-----LDRLHNKTEDDSMIRNWSHLG 446  
QY 680 DSSVPSSELSLPIAMEGLSTDTQT 701  
Db 447 VPIVPPSQAKPLKDRSAEET 468

RESULT 12  
T13960  
beige protein homolog - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
R:Accession: T13960  
R:Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.  
submitted to the EMBL Data Library, November 1998  
A:Description: Deletion in the beige gene of the beige rat due to recombination betwe  
A:Reference number: Z17837  
A:Accession: T13960  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA



A:Accession: T42730  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3788 <OR>  
 A:Cross-references: EMBL:AB020019; NID:dl241953; PID:dl035670; PIDN:BAA34688.1  
 A:Experimental source: strain DA; spleen  
 C:Genetics:  
 A:Gene: beige

Query Match 2.74; Score 108.5; DB 2; Length 3788;  
 Best Local Similarity 19.44; Pred. No. 31;  
 Matches 144; Conservative 98; Mismatches 267; Indels 235; Gaps 38;

QY 20 GSOLAVAGSGRAGADTCGWRMAAARPRCLVANCGVGPASRNSGLNITFYDNCCT 79  
 DB 651 GETLOGTLCGAGSGLPSPSYRF-----QGILP-----SSGSEDFLWDALEA 695  
 QY 80 YLNPVGNHVAADQNTISQYACH--DQAVVILHSPGALIEFLKGFVILEELSEG- 136  
 DB 696 YQNFIFQE--DRHNTQIASHICNLQKGNVIVQ-----KLNYIFNPVLQGV 743  
 QY 137 --KCCQILADPKQLNSFKRGMSQPFLLMKFET-DYFVKVVP-----FP 181  
 DB 744 ELVHCQOLSI-----TSAQTHSSQLKQYLPQVQIYILKTLIPILLKSRVIRDL 795  
 QY 182 SIKN-----ESNY-----HFF-FFRTRACDILLOPONLACKPFNPRMLNISQSGDMQ 229  
 DB 796 SCNGVHIIEIYLOGINSLSKAFETLIVSLGEOKRAAVPGV---DGLDIOELSSLS 852  
 QY 230 VSPDHAFHNGFPRFYLHYLKHGPFKTKCKOBTETISCLONVSPGDIIEIIVOD 289  
 DB 853 V-----GPSLEK-----QASTDPSLSLEK-----FYASLEDT 880  
 QY 290 TINTTRVMYALKPVHSPWAGPITRAVITVPLVVISAFATLFTVWCKRQKQENIYSHLDE 349  
 DB 881 DPKRTVQ-----DAHINTNIFCVAF-----LCVSKASDRESAN- 920  
 QY 350 ESSESTY--TAALPRELRPRKVFCLYSSKDGQNNHNV-----OCFAIFLODFCCEV 403  
 DB 921 ESDTSGDSTASEPLSHMLPRSL-----ENVLPSPCLHH-----958  
 QY 404 ALDINWEDFSLCREGQRENV--IQIHESOFI-----IVVCSKGMKYEVQKKNYKKGGRG 457  
 DB 959 AADIN--SNCR-----WIYMLNSVFQKQFHLGQFQVOCHE-LIFMIOKLFPSHTEDOG 1009  
 QY 458 SGKGELF-----LVASATAEKLRQAKOSSAALSXFIAVTFDYSCEDVPGILD-----507  
 DB 1010 RROGEMSVNKGGLARISOPENILAKEDVSSVTAPEPGFLKASDRVSELSQHMLPSAE 1069  
 QY 508 --LSTR-----YRLMNLPLQCSH--LHSDRGLQEPQONTRQG 542  
 DB 1070 QILATKSIPEAKTFMQESETCQIRLILLESILALCHLSARASQOKMELELP50-----1124  
 QY 543 SRNRYFRSGSLYVAICNNHOFIDEEP-----DNPEKQVFVFPPLRYREP 591  
 DB 1125 -----SUSLENILCLRLDLSQSKVAETELARPLEDALLRVALGNESADLDPGOT 1174  
 QY 592 VLKFDGSLVLDVNCVKPGPESDFCLKVEAAVIGATG-----PADSOHESQGLDGDGE 646  
 DB 1175 VTEKSHPS---EVLSPQGFSEAEEDSQCSKLKLEEEYEADSESNPEGETQDGV 1231  
 QY 647 ARPALQD-SAAALQD--LLHVTYKAG 667  
 DB 1232 ELPEAGSGSVIPNNLLESITHG 1255

## RESULT 13

T42730  
 Bassoon protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T42730  
 R:Dieck, S.; Samartti-Vila, L.; Languaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wez, J. Cell Biol. 142, 495-509, 1998  
 A:Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized  
 A:Reference number: 222249; NUID:98345363; PMID:9679147

A:Accession: T42730  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3942 <IE>  
 A:Cross-references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810  
 A:Experimental source: strain 129 SVJ  
 C:Genetics:  
 A:Map position: 9P1  
 A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1  
 A:Note: bassoon  
 C:Function:  
 A:Description: may be involved in cytomatrix organization at the site of neurotransmission  
 A:Note: component of the presynaptic cytoskeleton  
 C:Keywords: coiled coil; zinc finger

Query Match 2.74; Score 107.5; DB 2; Length 3942;  
 Best Local Similarity 19.14; Pred. No. 39;  
 Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;

QY 316 DNPQLCSLHSDHGLQEPQHTROGRRNYFRSKGRSLYVAIC-----NMHOFIDEE 570  
 DB 3535 DTCPQCS-----SHSMPDYQEHVKGDPRAHAYKREGYMLDDSHCWVSDSEAYHLGOEE 3589  
 QY 571 PDWFERQVFPHPPLPYRE-----PVLEKF-----DSGLVLDVNCCKPG 610  
 DB 3590 -TDWDR---PRDASDRFHGGHTVSSQKRGPARSHSYHDYDEPPEGLAPHD---EGG 3643  
 QY 611 PESDFCLVEAVLGTGATGPADSOHESRG-----GLDQDG-----EARP- 649  
 DB 3644 PGRH-----TSKRRHSHDGRHSGHAGEEPGRRAKPHARDMGHEARPH 3691  
 QY 650 -----ALDGSAAOLPLLHTV 664  
 DB 3692 PQASPAPAMKKGQGYPPSADYSQSRAPSAIHASESKKGSROAHTGPSALQPRADTQ 3751  
 QY 665 KAGSPDMRSDGYSDVSPSSLSLPLMEGLSTDTQETSSLTSSVSSSGIGEEPPAL 724  
 DB 3752 AQPOMQROAAPGQSQPPSSROT---PSGTASRQPTQOOOQOOQOGLGQQAPOQA 3808  
 QY 725 PSK 727  
 DB 3809 PSQ 3811

## RESULT 14

T30851

Lysosomal trafficking regulator, long splice form - mouse  
 N:Alternate names: beige protein homolog  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 24-Nov-1999  
 C:Accession: T30851  
 R:Barbosa, M.D.F.S.; Tcherenev, V.T.; Kingsmore, S.F.  
 submitted to the EMBL Data Library, September 1996  
 A:Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.  
 A:Reference number: 220903  
 C:Accession: T30851  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-3788 <BAR>  
 A:Cross-references: EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AC53011.1  
 A:Experimental source: strain C57BL/6J  
 C:Genetics:  
 A:Gene: Lyst  
 A:Map position: 1  
 C:Keywords: alternative splicing

Query Match 2.74; Score 107; DB 2; Length 3788;  
 Best Local Similarity 19.54; Pred. No. 40;  
 Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;  
 QY 20 GSOLAVAGSGRAGADTCGWRMAAARPRCLVANCGVGPASRNSGLNITFYDNCCT 79  
 DB 651 GETLOGTLCGAGSGLPSPSYRF-----QGILP-----SSGSEDFLWDALEA 695



QY 80 YLNPYKREVIADAQNTISYACH--DQAVTILSPGALGIEFLKGRVILEELKSG- 136  
 Db 696 YGSFVQE--DBLENTQIANHICNLKGNVYQH-----KLYNTFNPVLQGV 743  
 QY 137 ---RCCOOLILDKPKINSFRTHMESQPLMKKFT--DFYRVVP-----FP 181  
 Db 744 ELVHCQQLSIPS-----AQMCSQLKQYLPOEVLOIYLATLVLKSKRVHDFL 795  
 QY 182 STKN-----HFF--FRTACDILLQPDNLACKPFWKPRNINISQSGDMQ 229  
 Db 796 SCNGVHIIELNDIGRSHKAPETLIVSAGEQKQAAVLVY--DGLDIQQLPSLS 852  
 QY 230 VSFDRAPENFGPFYFLYHKLKHEGPKRRTCKEQTTETSCLLQNVSPGYIIELVDD 289  
 Db 853 V-----GPSLHK--QAQSDSPCLSRK-----PYASLREP 880  
 QY 290 TWTTRVMHVALKPVHSPWAGPIRAVAITVPLVVISAVATLFTVMCKKQENITSHLDE 349  
 Db 881 DPKKRTIH--QDVH-----INTINLFLCVAF-----LCYSKEADS--DR 916  
 QY 350 ESSESSTVIALPRERLRPRKPVFLCYSSKQGNHNVV---QCPAYFLQPCGCEVAL 405  
 Db 917 ESANESDTSGYDPSPELSHMLPCLSLD-----VLPSPCLLH-----AA 960  
 QY 406 DLWEDFSLCHREGQEWV--IQKHESQPI-----IVVCSKGMKYFVDRKNTKRGGRSG 459  
 Db 961 DLW-----SMCR-----WYMLNSVYKOFHRLGGFQVCHB--LIFMIQKFRSHTEQGR 1011  
 QY 460 KGEFL--LVAVSAIAELKRAQSSAALSKFIAYFYDSCGQVPGIL--DLSTK 511  
 Db 1012 OGEMSRNENELIRIS-----YPELTKGDVSSATAPDLGL 1048  
 QY 512 YRLMDN-----LPOLCSHLASRQGLQEPQHTRGSKRMVFRSKGRSLVAICN 562  
 Db 1049 RKSADSVRGFSQVPLTSAEQIVATE--SVPGE-----REAFMSQOSETSLQIRL 1098  
 QY 563 MEQFTDEEPQWKEQVPPHPPPLRYEPVLEKEFGSLVNDVCK----- 608  
 Db 1099 LESLLD-----ICLSARACQKMELEPLSGLSVENILCELREHLSQKVATE 1148  
 QY 609 -PGPESDECLVAEVLGA--TGPADS-----QHSQHGGLDQGPALDGSAAQPLILH 662  
 Db 1149 LAKPLDALLRVAGHNSADLPGDVAITEKSHPEELLSQPGDFSEAEQSCCLKIL 1208  
 QY 663 TVKAGSPDM--PRDSGIYSSVPSSLSPLMBGLSTQDTTSSLTSSVSSSGIAGE- 718  
 Db 1209 GEEGYEADSESNPEVDYQDGV---ELN--PEAGGFS--GSIVSNLENLTH---GEI 1259  
 QY 719 --EPPALPSKLLSSGCKADL 738  
 Db 1260 IYPEICMLGLNLLSASKALDOW 1281

## RESULT 15

D86477

Protein F1504.27 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: D86477

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakao, H.

A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; NCBI:21016719; PMID:11130712

A:Accession: D86477

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1638 &lt;STD&gt;

A:Cross-references: GB:AE005172; NID:98778345; PIDN:AAF79333.1; GSPDB:GN00141

C:Genetics:

A:Gene: F1504.27

A:Map position: 1

Query Match

Best Local Similarity 2.74; Score 106.5; DB 2; Length 638;

Matches 94; Conservative 63; Mismatches 175; Indels 153; Gaps 24;

QY 94 NITTSQACHQDVAVTILWSPGALGIEFLKGRVILEELKSGRQCOQILADPQLNLS 153

Db 275 DIKYGQVSCLODCIFVYHS-----KCATHEVNDGKELEWIESEDETDISP 322

QY 154 FRRTGMSQPLNKKFETDYKVVPPP-----SIKNSNTHPFFRTACDILLQPDNLAC 210

Db 323 FRNLG-----DGIKFKCHKHKLKNDGARDTEKQCRAC---IYP--IVS 364

QY 211 KPFWKPRNINISQHG--SDMQVSTDAHPNFGFRFYHLYKLKHESP--FKRTCKQBOT 266

Db 365 HQPTCKKCKNTSLHETVAGLSKRLDHALHN-----HTLILSPGPRFCCSACSRST 416

QY 267 TETTSCLLQNVSPGYIIELVDDTNTTRKVMHVALKPVHSPWAGPIRAVAITVPLVISA 326

Db 417 GFSYIC--SNKQODFVLVY-----RCISVLEYFIHRSHEH-----PIFISTS 457

QY 327 FATLFTVMCKKQENITSHLDESSE--STYTAA--LPRE---RLAPRPRKPVFLCYSSKDG 381

Db 458 YNSDEILCKVCKKRCGLCAHLQCTLCFTMCTYSCAIIPEITHYKFKDHPULSLCGESAD- 516

QY 382 QNHANVVOCPAYFLDQFCGCEVALDWDQFSLCRGQREWIQKHESQFIIVVCSGKMK 441

Db 517 ---NTWCEV-----CEKQDPKEWFTYCNK---CCITIH-----LHCIFGSS 553

QY 442 YEVDRKRYKKGGRSGKSGELFLVAVSAIAELKRAQSSAALSKFIAYFYDSCGSD 501

Db 554 VTH-----KPG-----SIFRDTYGVQV 570

QY 502 VPGILDISTYRLMDNLHLPOLCSHLSDRGLQEPQHTRGSRN--YFRSKSGSLT-V 558

Db 571 V-----FRNNSTHOLCYMCHNCTGL-----IFYGYRNATYYIHNHSTHRM 616

QY 559 AICNM 563

Db 617 IFCSL 621

Search completed: May 19, 2003, 09:25:43

Job time : 38.7988 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on May 19, 2003, 09:08:53 : Searchtime: 15:2893 Seconds  
(without alignments)  
2042.709 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPFLQCSVFETVACVACLG.....CQADLCGRSYDELEAVAPL753

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	7.7	866	1	I17R_HUMAN
2	306	7.6	864	1	I17R_MOUSE
3	135.5	3.4	502	1	I17S_HUMAN
4	126.5	3.2	718	1	Y502_CAEAL
5	115	2.9	998	1	EPB3_HUMAN
6	110.5	2.8	439	1	I17S_MOUSE
7	110	2.7	592	1	STB3_MOUSE
8	104	2.6	1463	1	PTP6_MOUSE
9	103.5	2.6	863	1	RGD2_HUMAN
10	102	2.5	859	1	ABR_HUMAN
11	101	2.5	1275	1	GNRP_HUMAN
12	100.5	2.5	794	1	RG65_HUMAN
13	99.5	2.5	783	1	ZF2_MOUSE
14	99	2.5	970	1	PSD1_YEAST
15	98.5	2.5	933	1	EPB3_MOUSE
16	98.5	2.5	1050	1	EX5B_CHLPN
17	98.5	2.5	820	1	CYMB_TRIGR
18	98	2.4	1845	1	Z236_HUMAN
19	97.5	2.4	984	1	EPB1_CHICK
20	97	2.4	984	1	EPB1_RAT
21	97	2.4	984	1	ABL_MVAR
22	96.5	2.4	746	1	EPB8_XENLA
23	96.5	2.4	903	1	MG09_HUMAN
24	96	2.4	424	1	H313_ARATH
25	96	2.4	560	1	E2K3_MOUSE
26	96	2.4	1114	1	CAEN_MOUSE
27	95	2.4	828	1	PRGR_HUMAN
28	95	2.4	933	1	AXO1_CHICK
29	95	2.4	1036	1	HM14_CAEAL
30	94.5	2.4	351	1	GTL1_RAT
31	94.5	2.4	770	1	ITB3_MCNVS
32	94.5	2.4	841	1	IS63_MCNVS
33	94.5	2.4	1011	1	M3K6_HUMAN

34 94 2.3 984 1 EPB1\_HUMAN P54762 homo sapien  
35 94 2.3 2044 1 SIF2\_DROME P91620 drosophila  
36 94 2.3 2044 1 SIF1\_DROME P91621 drosophila  
37 94 2.3 3224 1 RBP2\_HUMAN P49792 homo sapien  
38 93.5 2.3 806 1 RML1\_CHICK Q04982 gallus gall  
39 93.5 2.3 807 1 RML1\_COTJA Q34908 coturnix co  
40 93.5 2.3 901 1 A180\_MOUSE Q61548 mus musculu  
41 93.5 2.3 915 1 A180\_MOUSE Q05140 rattus norv  
42 93 2.3 429 1 EPC\_RAT P01855 rattus norv  
43 92.5 2.3 347 1 SH33\_MOUSE Q62421 mus musculu  
44 92.5 2.3 548 1 IDD\_MOUSE P98154 mus musculu  
45 92.5 2.3 684 1 FBL1\_CHICK O73775 gallus gall

#### ALIGNMENTS

##### RESULT 1

I17R\_HUMAN  
ID I17R\_HUMAN STANDARD; PRT: 866 AA  
AC Q96F46; O43844; 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17 receptor precursor (IL-17 receptor).  
GN IL17R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
EX MEDLINE=98035683; PubMed=9367539;  
RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,  
RA VandenBos T., Zappone J., Painter S.L., Armitage R.J.;  
RT \*Molecular characterization of the human interleukin (IL)-17  
receptor.\*  
RL Cytokine 9:794-800(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases  
CC -1- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
CC suggesting that additional components are involved in IL17-induced  
CC signaling.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- TISSUE SPECIFICITY: Widely expressed.  
CC -1- PTM: Glycosylated.

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EMBL: U58917; AAB90730.1;  
EMBL: BC011624; AAB11624.1;  
Genew: HGNC:5985; IL17R.  
MIM: 605461; -  
Receptor; Transmembrane; Signal; Glycoprotein.  
FT CHAIN 1 31  
FT SIGNAL 32 866  
FT DOMAIN 32 320 INTERLEUKIN-17 RECEPTOR.  
FT TRANSMEM 321 341 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 342 866 POTENTIAL.  
FT DOMAIN 810 818 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 49 49 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 206 206 N-LINKED (GLCNAC... ) (POTENTIAL).

FT CARBOHYD. 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD. 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD. 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT. 367 V -> N (IN REF. 1).  
 FT CONFLICT. 580 H -> R (IN REF. 1).  
 SQ SEQUENCE. 866 AA; 96131 MW; 28330BED303B0C9 CRC64;

Query Match 7.78; Score 310; DB 1; Length 866;  
 Best Local Similarity 23.18; Pred. No. 5.4e-16;  
 Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITKYNOC--TYLNPVKRVIADQNT-----ISQACHQ-----VATILMS-113  
 DB 49 NCTVKNSTCLDSDWHP-----ENLTPSPKDLQIOHFAFTQQDLPFAHIEWT 99  
 QY 114 -PGALGTEFLKGRVIELSEKQCOOLILKDPKQNSFKKNGESQPLANKFTD 172  
 DB 100 LQTOASILYLEGAELSVLQMINERLCVR--FEELSKLRHHRHWRFTSHFV-VDPOE 156  
 QY 173 TVFKV--VPPSTIKNESYHPEFFETACULLQPDNLACK---PFWKPRNL----- 219  
 DB 157 FEVTVHLPFPDGDPHQSKNLYPDCEHARKMTVTPCMSSGSLADP-NITVETLEAH 215  
 QY 220 ---NISQSDQVGFDPAPNFGFRFTYLYLKHGEPFKRYCKOQETTT 270  
 DB 216 QLRVSTFLMNESTHQILTSFPMENHSCFEMH-HIPAPRPEEFHQSNVTLRLNK 274  
 QY 271 SCLQNVSPDQYIIELVDOT---WTRKVMYALXPHVSPWAGPIRAVAITVPLVVISAF 327  
 DB 275 GCRHVOIQPFSSCLNDCLRHSAVSCPEMDPEPIPYMPLVYFVITGISILLVG 334  
 QY 328 ATLTVACRKQOENYIHLDEESSESTYTAALPRELRPRP---KYFLCYCKDQGN 383  
 DB 335 SVILLVCMTRWLAGPGS---EKSDDTKTDLGLPVADLPPPLKPKRWIILYA-DHPL 390  
 QY 384 HNVVOCFAVFLDQCGCEVALDWDPSLCREGQENV---IQKHESQFLVVCCKG 439  
 DB 391 TVDVVLAFAQLLTACGTEVALDLEQALISGAVMTWVQKQEVESKNIIVLCSEK 450  
 QY 440 KMYFVKNKTHKGGG-----RSGGGEFLVAVSAIAKLRQAKOSSAALSKRIA 491  
 DB 451 TR---AKWALLRGAPVRLCRDHGAPVGDGLFTANNHLLPDFR-----PACGTIVV 501  
 QY 492 YTF-DYCEGDVPIILDSTYRLMDNLPQLCSHLSDHDEGLQEPQHTQCG--SRNRYF 548  
 DB 502 CYFSECDGVDPDLFGAAPRIPLMDRFEV--YFRIQDLEMFQGMHVRGELSGDNTL 559  
 QY 549 RSKGRSLYVAICNHQFIDEPDWE-----KQFVPPHPPPLRYREPVLKFDGSL 600  
 DB 560 RSPGGROLRAALDRFQWQVCPWFCEENLYSADDODAPSLDEEV-FEELPLPP-GTGI 617  
 QY 601 VLNDVCKPGPSDFCLKVEAALVGTAGPADSQHE-----SQRGG 640  
 DB 618 VKRAPLYRE-PGSOACLAIDPLVEEGAAVAKLEPHLPQPGQAPQPLHTVLAERGA 676  
 QY 641 LDQGEARPAIDGSA---ALO-----PLHTVKAQSPMDRDSGIYSSVPSSELSLP 691  
 DB 677 LVAAVEFGPLADGAAYRALAGEACEAPLLGSPGAG-----RNSVLF---LEVPDPS 727  
 QY 692 LMEGLSDTOTSSLTSESYSSSSGLGEPEPPALPSKLLSGCKADIGC 740  
 DB 728 L--GSSTPMASPOLLPEDVR-----EHLEGLMLSLFQSLSCQAQGC 768

## RESULT 2

IL17R\_MOUSE  
 ID IL17R\_MOUSE STANDARD; PRT; 864 AA.  
 AC Q60943.  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17 receptor precursor (IL-17 receptor).  
 GN IL17R.

OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=thymic lymphoma;  
 RX MEDLINE=96111968; PubMed=8777746;  
 RA Yac Z., Fanslow W.C., Seidlin M.F., Rousseau A.M., Palinter S.L.,  
 RA Comeau M.R., Cohen J.I., Spriggs M.K.;  
 RT 'Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a  
 RT novel cytokine receptor'.  
 RL Immunity 3:811-821(1995).  
 CC -FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
 CC suggesting that additional components are involved in IL17-induced  
 CC signaling (By similarity).  
 CC -SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
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 DE EMBL; U31993; AAC52357.1;  
 DE MGD; MGI:107399; IL17r.  
 KW Receptor; Transmembrane; Signal; Glycoprotein.  
 FT SIGNAL 1 31 POTENTIAL.  
 FT CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.  
 FT DOMAIN 32 322 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 323 343 POTENTIAL.  
 FT DOMAIN 344 864 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 809 814 POLY-GLU.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 7.68; Score 306; DB 1; Length 864;  
 Best Local Similarity 22.58; Pred. No. 1.1e-15;  
 Matches 189; Conservative 128; Mismatches 319; Gaps 43;

QY 40 GWRM-----KAAARPEL-----CVANEGYGPASRNSGLNITKYNCTTYLNPVK 86  
 DB 17 GMLLLLVLPAGRAPSLDFPAPVCAQEGLSCHRVKNSCLDSDSNHFKNLTSSPKNI 76  
 QY 87 HYIADAQNTISQACHQVAVT-ILMS-PGALGTEFLKGRVIELSEKQCOQ--- 141  
 DB 77 YI-----NLSVSTQHGELVPLHVEWTQDASILYDEGRELSTVQLATNERLCVRFQ 131  
 QY 142 ---LLIKDPKQNSFKRTGMSQPLNMFETDYFVKYVPPSPKKNESYHPEFFETRAC 199  
 DB 132 LSLQLHHRKWRFSF-----SHEFVDPQOYETVTVHLPKPIPDGDPNKHKILFVDC 185  
 QY 200 D---LLQPDNLACKPFWKPRNLNI---SQH-----GSDMQV 230  
 DB 186 EDSKMKNTTSCVSSGSLADP-NITVETLDTQHLRVDFTLWNESTPYOVLESFSDSENH 244  
 QY 231 SFD-----HAPNPGFRFTYLYLKEH---GPKFKTKQEQETTTSCLL 274  
 DB 245 CFTVYVQIIPAPQREFFHQANVTPLSKFWCHHVVQVDF-PSCLND-----CLR 296  
 QY 275 QNVSPGDYIIELVDDTNTKVMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAPATL 330  
 DB 297 HAVTVPCPVI-----SMT-----VPKPVADYIPLWYGLITLIAI-----LLVGSVIL 341  
 QY 331 FTVACRKQOENYIHLDEESSESTYTAALPRELRPRPRKRYFLCYCKDQGNHNVQC 390



QY 356 YTTAAL-----PRELR-----PRKFLCYSKDQNHNM 386  
 DB 289 GWPLLSLLVAVVAVAGVILWREIRIKATSEITLLPIKVLVYPSICFHH-- 346  
 QY 387 VVQCFAYFLDQCGEVALDNEFSLCHREGRENVOKIHESQFIIVVCSGKGYFDK 446  
 DB 347 TICITFEFLQHCRESVILEKWKIKAEQVQVATQKADKRVVFLISNDVNSVCDG 406  
 QY 447 KNYKHGGGSGSGELFVAVSAIAEKLRQAKSSAALSKATYIFDYSCEGDFGIL 506  
 DB 407 TCGSBSGSPENQ-DLFPFLNFCSDLR-----SQHLKRYVYVYFREDIKDYNAL 460  
 QY 507 DLSTKRYLMDNLPOLCSHL 525  
 DB 461 SVCPKYLMDATATACAE 479

RESULT 4  
 ID YS02 CAEL STANDARD; PRT; 718 AA.  
 AC Q10128; 1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE Hypothetical 81.6 kDa protein F56D1.2 in chromosome II precursor.  
 GN F56D1.2  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Chiswick S. Wilson R.  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

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 CC  
 CC EMBL; U39997; AAA81100.1;  
 DR Wormpep; F56D1.2; C801970.  
 KW Hypothetical protein; Transmembrane; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 718  
 FT TRANSMEM 373 393  
 FT SEQUENCE 718 AA; 81622 MW; 4289E056288417AA CRC64;  
 Query Match 3.28; Score 126.5; DB 1; Length 718;  
 Best Local Similarity 21.18; Pred. No. 0.064;  
 Matches 84; Conservative 64; Mismatches 149; Indels 94; Gaps 19;

QY 363 RERLRPRP-----KFLCYSKDQNHNMVYVQCFAYFLQDFCGEVALDNEFDS 412  
 DB 398 RDKVRSEVRNIALTEFYKVMVYAD-DNDLHTDCVKRLVNLNRCASCDPVFLEKIT 456  
 QY 413 LCRCGQRENVOKIHESQFIIVVCSGKGYFDKRYKKGSGSGKGLFVAVSAIA 472  
 DB 457 AEQIVPSRWLVQISSLKFLIVVSDCAEKILDTSEATHTQVQAPFPADLFGPMENI- 515  
 QY 473 ELKQAKQSSAALSKATYIFDYSCEGVP---GILDSTKRYLMDNLPOLCSHLISRD 529  
 DB 516---IRDTNFPKARKYAVRNFNS--PHVPPNIAIMLPT-FILPEQPAQLTAFIARVE 570  
 QY 530 HGLQEPQHTGRRNRNFRYSKSGSLY---VAICNKHQFIDEEPWFKEQFVP----- 580  
 DB 571 E-----TERANYTONISEAQITHENWLCASRMNSFFVRNPNNWLETRKPKDELA 619

QY 581 FHPPLRYREPVLKFEGLVLDVNMCKPGSPDCLKVAALVGLGATGPADQSHQSBGG 640  
 DB 620 LH---LKRSPVPIPT-----EED---RIAASIKYLVPPQALVDSO--- 657  
 QY 641 LDQGEARPALDGSMAALQPLHTVKAAGSPDM--PDGSIYDSSVSPSELSPLMECLST 698  
 DB 658 -DED-----DVDLQP---HASHQNPILLPLPEQCG-----PDSO-----SD 690  
 QY 699 DQETSSLTSSVSSSGLGEEPPALPSK 727  
 DB 691 SESDSSSESESDNEG---EDPTIVVK 716

## RESULT 5

ID EPB3 HUMAN STANDARD; PRT; 998 AA.  
 AC P54753;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE Ephrin type-B receptor 3 precursor (BC 2.7.1.112) (Tyrosine-protein  
 DE kinase receptor HEK-2).  
 GN EPB3 OR ETK2 OR HEK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93390963; PubMed=8397371;  
 RA Boehme B., Holtrich U., Wolf G., Luzius H., Grzeschik K.-H.,  
 RA Streibhardt K., Ruebner-Waigmann H.;  
 RT \*PCR mediated detection of a new human receptor-tyrosine-kinase, HEK  
 RT 2.;  
 RL Oncogene 8:2857-2862(1993).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO  
 CC EPHRIN-B1 AND -B2.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: UBICUITOUS.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X75208; CAA53021.1;  
 DR HSP; P29323; I84F.  
 DR Genew; HGNC:3394; EPB3.  
 DR MIM; 601839;  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003962; FNIII\_repeat.  
 DR InterPro; IPR001560; SAM.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR001426; Yrase\_receptor.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR Pfam; PF01404; EPH\_lbd; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.

DR ProDom: PD001495; Ephrin\_receptor; 1.  
 DR SMART: SM00060; FN3; 2.  
 DR SMART: SM00454; FN3; 1.  
 DR SMART: SM00219; TYKIC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE: PS00105; SAM\_DOMAIN; 1.  
 DR Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 33 POTENTIAL.  
 FT CHAIN 1 34 998 EPHRIN TYPE-B RECEPTOR 3.  
 FT DOMAIN 34 559 EXTRACELLULAR POTENTIAL.  
 FT TRANSMEM 560 580 POTENTIAL.  
 FT DOMAIN 581 998 CYTOPLASMIC POTENTIAL.  
 FT DOMAIN 199 336 CYS-RICH.  
 FT DOMAIN 337 448 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 449 544 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 633 896 PROTEIN KINASE.  
 FT DOMAIN 925 989 SAM.  
 FT SITE 996 998 PDZ-BINDING MOTIF (POTENTIAL).  
 FT NF\_BIND 639 647 ATP (BY SIMILARITY).  
 FT BINDING 665 665 ATP (BY SIMILARITY).  
 FT ACT\_SITE 758 758 BY SIMILARITY.  
 FT MOD\_RES 608 608 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 614 614 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 792 792 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 942 942 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CARBOHYD 351 351 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 445 445 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT SEQUENCE 998 AA; 110286 MW; 57826397CC61103 CRC64;  
 Query Match 2.9%; Score 115; DB 1; Length 998;  
 Best Local Similarity 19.0%; Pred. No. 0.78; Indels 250; Gaps 42;  
 Matches 158; Conservative 122; Mismatches 301;  
 QY 35 GADTGWKMAARPLC-----VANEGVGA-----SRNSG-----LYNIFK 73  
 DB 267 GACTCATGEPKAPKSCPCPPGSKAKGEGPCLPSPNSRTTSPAAICICHNNFR 326  
 QY 74 YDN-----CTYINPVGHVITADQNTTISQACHDVAVTILMS-PGALGIEFLKGR 126  
 DB 327 ADSADSACTTVPSP-PRGVLSNV-----NETSLIENSEPRDLGVDDLLYN 374  
 QY 127 VILEELKSG-----RCCQLILADPKOLNSSEKRTGMSQPLNMFETDYFVKKVPP 181  
 DB 375 VICKKCHGAGSACSCDDNVEFVPGGLSEPRVETS-----HLLARTYTFEQAVN 429  
 QY 182 STKSNVHPFFETTRACDLILQDNLACFPKPRNLMSQSDMOVSDIAPHNFG 241  
 DB 430 GYSGKSLPPRYAAVITNQAPSEV-----PRLHSSGSGSLTSWAPERNP- 481  
 QY 242 RFFLYHKLKGGPP-KRTCKQEGTFTTSCILQWSP-GDYITIELVDNTTRKVHY 299  
 DB 482 --VILDYEMKT--FKSGIASHVTISQMSVQDLGLRDARYVQV-----BARTVAGY 531  
 QY 300 A--LAPVH--SPWAGPIRAVATVPLVWISAFATL-----FTVMCKKQQENIYS 345  
 DB 532 GQYSPAEFETTSERGSAQQLQOLPLTVGSATAGLVFVAVVAVIATVLRQRH--- 587  
 QY 346 HLDSESSSTTTAALPRELRPRKPKYLCYSSKDGONMNVQCFAYFLDQFC-CCVA 404  
 DB 588 -----GSDSEYTEL-QYIAPGHVYIDFFYEDPN-EAVREFAREIDVSCVKEEV 638  
 QY 405 LQWDFSLCREGQRENTQKTHESQFTIVVCSKGMKFTVDKKNKKGGRSGGKGLF 464  
 DB 639 IGAGEFGEVCR-----GRLKQFGREVF 661  
 QY 465 LVAVSAI-----AEKLRQAKSSAALSKEFATVFDYSCGDVPGTLOLS---TKYR--- 513  
 DB 662 -VAITKLKVGTYERQRDRDPLSEASINGOF-----DHPNIIRLEGWTKSPVMI 709

QY 514 ---LADNLPOLCHLSHRDGLQEQHT-----RQSRNRY-FRKSQR 554  
 DB 710 LTFEMNG-ALDSFLKND-----GQFTVQLVGMRLGIAGMKYLSKNVYHDLAAR 762  
 QY 555 SLTV---AIC-----AMHOFIDEPDFERQFVPPHP-----PLRYREP---VLEKFD 597  
 DB 763 NLYNSNLVKVSDGLSRFLDDPS-----DPTVTSSLAGKIPITWTAPEAIATKFT 816  
 QY 598 S-----GLVLDNVCKPGPSDFCLKVAANVLGATGPAQSQHSQHGQLDQCEARPA 650  
 DB 817 SASDVMSVGTVMVEVS-----YGERPTWMSNQDVINAVEQDYLPP 860  
 QY 651 LDGSAALQPLHVRKAGSDMPDSDGTYDS-----SVPSSELSLPMSEL 696  
 DB 861 MDCPTALHOLMLQWDRDLNRPKESQIVNTLKLIRNAASLKVIAQSGASQPLDRT 920  
 QY 697 STDQTESSTESVSSSGLSGHEPPALPSKILLSGCKADLCGRSTYDEL 747  
 DB 921 VPDYITFTTVDWLDIAK-MGRK-----ESFVSAGFASFDLYAQMTAEDL 965  
 RESULT 6  
 IL17s\_MOUSE  
 ID IL17s\_MOUSE STANDARD; PRT; 499 AA.  
 AC Q9JIP3; Q9JIP2;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog 1) (IL-17R1) (IL17R1) (IL-17R).  
 GN IL17B OR EVI27.  
 OS Mus musculus (mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=20273223; PubMed=10815801;  
 RA Tian E., Sawyer J.R.; Largaespada D.A., Jenkins N.A., Copeland N.G.,  
 RA Shaughnessy J.D. Jr.;  
 RT "Evi27 encodes a novel membrane protein with homology to the IL17 receptor".  
 RL Oncogene 19:2038-2109(2000).  
 CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Liver and testis. Expressed at lower level in kidney and lung. Expressed in selected T-cell, B-cell and myeloid cell lines.  
 CC -1- MISCELLANEOUS: EVI27 is a common site of retroviral integration in BXH2 murine myeloid leukemias, localized near the IL17B gene. Proviral integrations result in increased expression of IL17B on the cell surface.  
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 CC EMBL: AF208108; AAF86049.1;  
 CC EMBL: AF208109; AAF86050.1;  
 CC MGD: MGI:1355292; IL17br.  
 CC Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 499 INTERLEUKIN-17B RECEPTOR.

FT DOMAIN 18 286 EXTRACELLULAR (POTENTIAL);  
 FT TRANSMEM 287 307 POTENTIAL;  
 FT DOMAIN 308 499 CYTOPLASMIC (POTENTIAL);  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC) (POTENTIAL);  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC) (POTENTIAL);  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC) (POTENTIAL);  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC) (POTENTIAL);  
 FT VARSPLIC 163 218 LHMVTKRQCTEAGSDWPDITACKKRAVEVNTTNPPL  
 FT :GNRTILLQPDITGG--TRENTVSGVFPAAKQGLRI  
 FT :SAFFLQPPGPDGVILPQPLASLDFVFLT (IN  
 FT :ISOFORM 2).  
 FT VARSPLIC 219 499 MISSING (IN ISOFORM 2).  
 FT SEQUENCE 499 AA: 55617 MW: C66440430E3C31P3:CRG64;  
 Query Match 2.8% Score 110.5; DB 1; Length 499;  
 Best Local Similarity 24.1% Pred. No. 0.66;  
 Matches 40; Conservative 27; Mismatches 82; Indels 17; Gaps 4;  
 QY 355 STYTAALPRERLRPRKPVFLCYSSKQGNHNVQCFAYFLQDFGCEVALDWDPSLC 414  
 DB 314 STKTSFPLSLKLVLPVSEICFHH--TVCRFTDFLONTSEVILENMOKKIA 371  
 QY 415 REGOREWVIOKTHESQFIIVVCSKMKYFVOKKNTKKGSGSGGKGEFLVAVSAIAEK 474  
 DB 372 ENGFWLITOKADKVVLPSPVTLCDSCAGHNGSARENSQ--DLFPLFLPQSD 430  
 QY 475 LQAQSSSNAISKIAYFDYSCGDPGCLDLSTKYRMDNLPQ 520  
 DB 431 F--SSQTHLEKYLIVIL-----GGADLKGDNALSVCPO 462  
 RESULT 7  
 STB3\_MOUSE  
 ID STB3\_MOUSE STANDARD; PRT: 592 AA.  
 AC Q60770;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Syntaxin binding protein 3 (UNC-18 homolog 3) (UNC-18C) (MUNC-18-3).  
 GN STXBP3 OR UNC18C  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=95197608; PubMed=7890715;  
 RA Tellam J.T., McIntosh S., James D.E.;  
 RT "Molecular identification of two novel Munc-18 isoforms expressed in  
 non-neuronal tissues."  
 RL J. Biol. Chem. 270:5857-5863(1995).  
 [2]  
 SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c; TISSUE=Brain;  
 RX MEDLINE=96411662; PubMed=8824310;  
 RA Gengyo-Ando K., Kitayama H., Mukaida N., Ikawa Y.;  
 RT "A murine neural-specific homolog corrects cholinergic defects in  
 Canorhabditis elegans unc-18 mutants."  
 RL J. Neurosci. 16:6935-6942(1996).  
 CC -1- TISSUE SPECIFICITY: USBIQUITOUSLY EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE STXBP/UNC-18/SECI FAMILY.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: U19521; AAC69913.1;  
 CC EMBL: D30798; BA19478.1;  
 CC GCD; MG1:107362; Strp3.

DR InterPro: IPR001619; Sec1-like.  
 DR Pfam: PF00995; Sec1.1.  
 KW Protein transport.  
 SO SEQUENCE 592 AA: 67942 MW: 7874B71DE107871A CRC64;  
 Query Match 2.7% Score 110.0; DB 1; Length 592;  
 Best Local Similarity 18.5% Pred. No. 0.92; Indels 188; Gaps 22;  
 Matches 93; Conservative 64; Mismatches 157;  
 QY 331 LWISAPATLFTVMCRKQO-----ENIYSHDESSSTTTAALPRELRPRK 371  
 DB 34 IMLEDEFTTKLSSCKMTDLLEGITVIENIYKNEPVRMKALYF-----ISPTPK 86  
 QY 372 VFCTYSKQGNHNVQCFAYFLQDFC-----GCE----- 402  
 DB 87 SVDCFRLDFGSEKSKYKAAVIYFTDFCPDLSFNKIKASCSIRKCKEINISFIPOESQ 146  
 QY 403 VALDLWEDFSLC-----REGOREWVIOKTHESQFIIVC-----SKMKY 442  
 DB 147 VTLVDPDAFYCYSPDPSNASRKEVVMNAEQ--IVTVCATLDENPGVRYKSKPLDNA 204  
 QY 443 -----FVKK--NKK--HGGGSGSGKGEFLV-----AVSALAELKRAQKSSAALS 487  
 DB 205 SKLAQLVFNKLEDTYRDEKGLNGKTSQQLIDRGDFPVSVLHEL----- 252  
 QY 488 KFIATVFD-----YSCGQ--DWPGIL-----DLSTKYR-----LMDNLPOLCSHLH 536  
 DB 253 TFQAMAYDLLPIENTYTKYTDKKEAVLEEDDLAVRVYRHRHTIIVLEELIPKLMKEIS 312  
 QY 527 SRDGLQEPQHTROGSRNRYFRSKSGSLYVAICNMHOFIDEEPWFQKQVFFHPPL 586  
 DB 313 STK-----KATECKTSLSLTQLMKMPHFRIQISKQVV-----HL 348  
 QY 587 RYREPVLKFF-----DSGLVLDVNMCKPGPSDFCLKVE 620  
 DB 349 NLADCMNFKLNIEKLTQDLAGLTDAEGRVDSNLEVLPLVLL--NKNHNCCKIR 406  
 QY 621 AAVLGATGPADESQHSQGLDQGEARPALDGSAAALQPLLTVTAKGSPDMPRD--SGIY 679  
 DB 407 AVLLYIFGNGTEEN-----LDRLHNKVEDSDSMDIRNWSHLG 446  
 QY 680 DSSVPSSELSLPLAGGLSTQDT 701  
 DB 447 VPIVPPSQQAFLRKDRSAET 468  
 RESULT 8  
 PTP6\_DROME  
 ID PTP6\_DROME STANDARD; PRT: 1462 AA.  
 AC P16620;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase DTPP precursor (EC 3.1.3.48) (Protein-  
 tyrosine phosphatase phosphonolase).  
 GN PTP69D OR DPTP.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=90046860; PubMed=2554325;  
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 and Drosophila."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 CC -1- FUNCTION: IT IS POSSIBLE THAT DTPP IS A CELL ADHESION RECEPTOR.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2O) -> protein  
 tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.





CC lymphoid tissues.  
 CC -1- INDUCTION: By 12-O-tetradecanoylphorbol-13-acetate (TPA) in  
 CC promyelocytic HL-60 cells.  
 CC -1- SIMILARITY: CONTAINS 1 RAP/RAN-GAP DOMAIN.  
 CC  
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 CC  
 CC EMBL; M64788; AAC60232.1;  
 CC Genbank; HGNC:9858; RADICAL.  
 CC MIM; 600278;  
 CC InterPro; IPR003109; GTPase\_LGN.  
 CC InterPro; IPR000331; Rap\_GAP.  
 CC Pfam; PF02145; Rap\_GAP; 1.  
 CC Pfam; PF02188; GoLoco; 1.  
 CC SMART; SM00390; GoLoco; 1.  
 CC GTPase activation; Membrane.  
 CC KW DOMAIN 210 397  
 CC FT  
 CC SQ SEQUENCE 663 AA; 73391 MW; 3703B7CC60340ADA CRC64;  
 CC  
 CC Query Match 2.6%; Score 103.5; DB 1; Length 563;  
 CC Best Local Similarity 19.5%; Pred. NO. 3.4;  
 CC Matches 143; Conservative 80; Mismatches 262; Indels 247; Gaps 33;  
 CC  
 CC 167 MKETDYKVKVPPPSIKNESNYHFFETFRACDLALPD----- 206  
 CC 21 LATEEDY-----IPYGV-----HEVLGREGPPPLTLPOFGYWIETGTHETTSIPETE 70  
 CC  
 CC 207 -----MLACKP-----FWKPRNLNISQSGSDMOVSFDRAPHNPGFFFLYHK 249  
 CC 71 PIQSPPTVKLECNPARIYRKHFLGKEFN-----YLSLDTA-----LGLHVFSLAYD 119  
 CC 250 L-----KHEGPKKTKCKQBTETTSCLLQNSGDXIIEVLVDNTNTRVHYALKPVH 305  
 CC 120 VIGDQEHLLRLTKCTHYDIPISCLTEFPNVQMAKLVCEVDVDR-----FYPVL 173  
 CC 306 SPWAGPIRAVAVTFLWLS-----APATLFTWCKRQKQENYSHLDESESESTTAALP 362  
 CC 174 YPAS-----RLVTFDEHLSNNFAGVITOKLGTSEEE-----LFTNEESPAFVELE 225  
 CC 363 RERLRPRKVLFLYCSKQGNIMNVQCFAYFLQDPCGCEVALDLNE-----DFSLCR-- 415  
 CC 226 -----FLQKVK-----LQDFKFGRLDVTGQGTGVSYCNFR 260  
 CC 416 -----EGREWVIOKIHESOFILVVCCKMFIYDK-----KNYK 450  
 CC 261 NKEIMFHVSTKLPTTGDAAQLQRRHIGNDIVA-----VFQENTPFPVDMIASNFL 314  
 CC 451 H-----KGGRGSGKGLFVAVSAIE-----KLQKAKOSSSAALSKEIA 491  
 CC 315 HAVVVQAEKG-----PDGLIKVSTARDVPPFPPLDPNAVFKGPEQELTKLIN 371  
 CC 492 VTFDYSC-EGDVGILDLSTKYLMDMLPOLCSHLHSRD-HGLQEPQGHTRGSRNRP- 548  
 CC 372 A--ETACTYAKKFAKLETRAALETLYEEL-HINSQSMGLGDEEDKENSQGGGFF 428  
 CC 549 -----RSKGRSL-----TYAICNMHQFIDEPPWFE-----KQVFPFPPPLR 587  
 CC 429 ESFKVRVRSRSQMDANGLSNKKNTVSTSHSGSPAPNPNPLAKAIGLSLVPGKSPTRK 488  
 CC 588 YREPLEKFSGLVANDVCKPGPESDFCLKVEAVLGNATGPDSQSHOSHGGLDQGEA 647  
 CC 489 KSGPPGSRSSATGIENI-----QEVQERESPACQKTP-DSGHVSEPKSE----- 535  
 CC 648 RVALDGSAAQPLHTVTKAGSPMDPRDSGIYDSVPSELS-----LPLMEGLSTQDTE 702  
 CC 536 -----NSSTQSGSPENPTTKRAETAQRAEALKDFSRSSASSFASVVEETGVGDTG 591

CC 703 TSS-----LTSSVSSSG-----LCSEPPPALPSKL 728  
 CC 592 LESVSSSGTPEKRDSTFYLTWLEDVSTTSGGSSPSPSRPHDPACKLGPACPEIKQL 651  
 CC 729 LSSGSCRADLGC 740  
 CC 652 EASQERAPQLGC 663  
 CC  
 CC RESULT 10  
 CC ABR\_HUMAN  
 CC ID ABR\_HUMAN STANDARD; PRT; 859 AA.  
 CC AC Q12979; Q13693; Q13694;  
 CC DT 15-JUL-1999 (Rel. 38, Created)  
 CC DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Active breakpoint cluster region-related protein.  
 CC GN ABR.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 CC OX NCBI\_Taxid:9606;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC Tissue-Hippocampus;  
 CC RX MEDLINE=34086546; PubMed=8262969;  
 CC RA Tan E.-C., Leung T., Manser E., Lim L.;  
 CC RT "The human active breakpoint cluster region-related gene encodes a  
 CC brain protein with homology to guanine nucleotide exchange proteins  
 CC and GTPase-activating proteins";  
 CC RL J. Biol. Chem. 268:27291-27298(1993).  
 CC RN [2]  
 CC RP SEQUENCE OF 39-859 FROM N.A. (LONG AND SHORT FORMS).  
 CC RC Tissue-Fibroblast;  
 CC RX MEDLINE=93352461; PubMed=8349582;  
 CC RA Heisterkamp N., Kaartinen V., van Soest S., Bokoch G.M., Groffen J.;  
 CC RT "Human ABR encodes a protein with GAPrac activity and homology to the  
 CC DAL nucleotide exchange factor domain";  
 CC RL J. Biol. Chem. 268:16903-16906(1993).  
 CC RN [3]  
 CC RP SEQUENCE OF 436-597 FROM N.A.  
 CC RX MEDLINE=90067847; PubMed=2587217;  
 CC RA Heisterkamp N., Morris C., Groffen J.;  
 CC RT "ABR, an active BCR-related gene";  
 CC RL Nucleic Acids Res. 17:8821-8831(1989).  
 CC CC -1- FUNCTION: GTPASE-ACTIVATING PROTEIN FOR RAC AND CDC42. PROMOTES  
 CC THE EXCHANGE OF RAC OR CDC42-BOUND GDP BY GTP, ~~WHEREAS~~ ACTIVATING  
 CC THEM.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: HIGHLY ENRICHED IN THE BRAIN. MUCH WEAKER  
 CC EXPRESSION IN HEART, LONG AND MUSCLE.  
 CC -1- SIMILARITY: CONTAINS 1 DAL-HOMOLOGY (DH) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.  
 CC -1- SIMILARITY: STRONG, TO HUMAN BCR.  
 CC  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; 001147; AAC50063.1;  
 CC EMBL; L13704; AAC37519.1;  
 CC EMBL; L13705; AAC37518.1; ALT\_INIT.  
 CC Genbank; HGNC:81; ABR.  
 CC MIM; 600365;  
 CC InterPro; IPR000008; C2.  
 CC InterPro; IPR001331; GDS\_CDC24.



QY 126 RVILEELKSGROCOOL-TLKD---PRLNSFKRTGME---SOPFLANKPKTDYFKV 176  
 Db 243 QVFSKLEAEATVOQLHLVNNELRPLRLMASSKKPPTHDVSIFLAS--ETIMFLH 300  
 QY 177 VVPFSSIKNSYHFFRTRACDLLOPDMLACKPFWPRLNISO---HGSDMQVS 231  
 Db 301 QITGCLARISSTPVLADLILLP-----MLNITQFVNRHQSILQI- 346  
 QY 232 FBAHPNPGFFVLYLKLHSGPFRKTKQBTTFETSCILQNVSPGDIYELVD--- 288  
 Db 347 LAHQONDFDKLHYEARPD-----C-BERTLETFLVPMFQIP-RYILTHDVL 397  
 QY 289 ---DNTTKVMYKALVHSPWAGPIRAVAITVPLVLSAFATLFTVWCKKQSNIS 345  
 Db 398 HTPHEVERNSLDYA-----KSKLELSR 421  
 QY 346 HLDSESSSTYTAALPRRLRPRKPVLCYSSKDGQNNMVVOCFAIFLQDFGCEVAL 405  
 Db 422 INHDSVSETEIRANLAIRM-----IIE-----GCEILL 451  
 QY 406 DLWEDF-----SLRCQRENVQIKHESQFIIVWCSGM 440  
 Db 452 DTSQTFVROGLIOPVMSKGIKTRGLGSLSEKGEKQCLFSKH-----HICTRGS 506  
 QY 441 ---KYVDKNT-----KHGGG-----RSGKGLFIVA 467  
 Db 507 GKKLHLTRNGVISLIDTLLEPSTEEAAGSQDIDHLDKFGVGPDPSPPTVILVA 566  
 QY 468 VSAIAKLQAKQSSAALSKFIAYFDYSGEDVPGIILSTIKYLMNLPOLCSHLHS 527  
 Db 567 SS-----ROEKAWTSISOCVD---NIRCNGLMNAFEENSKV---TVPMKI 608  
 QY 528 RDHGLQEPQHTROGSRNRYFSKRSGLY 557  
 Db 609 -----KTRBSTREAM-SRSDASLY 628  
 RESULT 12  
 R6G6 HUMAN  
 ID R6G6 HUMAN STANDARD; PROT: 974 AA.  
 AC Q43182; Q43437; Q9P1B3; Q9UK81; Q9UK82;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 18-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rho-GTPase-activating protein 6 (Rho-type GTPase-activating protein  
 RhoGAP6-1).  
 GN ARHGAP6 OR RHO GAP6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. REVISIONS, FUNCTION, SUBCELLULAR LOCATION, AND  
 RP ALTERNATIVE SPLICING.  
 RC TISSUE=fetal kidney;  
 RA MEDLINE=20164286; PubMed=10699171;  
 RA Prakash S.K., Paylor R., Jenna S., Lamarche-Vane N., Armstrong D.L.,  
 RA Xu B., Mancini M.A., Zoghbi H.Y.;  
 RA "Functional analysis of ARHGAP6, a novel GTPase-activating protein for  
 RT RhoA";  
 RL Hum. Mol. Genet. 9:477-488(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=98086484; PubMed=9417914;  
 RA Schaefer L., Prakash S.K., Zoghbi H.Y.;  
 RT "Cloning and characterization of a novel rho-type GTPase-activating  
 RT protein gene (ARHGAP6) from the critical region for microphthalmia  
 RT with linear skin defects";  
 RL Genomics 45:268-277(1999).  
 CC -1- FUNCTION: GTPASE ACTIVATOR FOR THE RHO-TYPE GTPASES BY CONVERTING  
 CC THEM TO AN INACTIVE GDP-BOUND STATE. COULD REGULATE THE  
 CC INTERACTIONS OF SIGNALING MOLECULES WITH THE ACTIN CYTOSKELETON.  
 CC PROMOTES CONTINUOUS ELONGATION OF CYTOPLASMIC PROCESSES DURING

CC CELL MOTILITY AND SIMULTANEOUS RETRACTION OF THE CELL BODY  
 CC CHANGING THE CELL MORPHOLOGY.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1, 2, 3 (SHOWN HERE), 4 AND 5;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL  
 CC MUSCLE FOLLOWED BY RETINA, LYMPHOBLAST, PLACENTA, LUNG, BRAIN,  
 CC PANCREAS AND LIVER.  
 CC -1- DISEASE: DEFECTS IN ARHGAP6 MAY BE A CAUSE OF MICROPHthalmia WITH  
 CC LINEAR-SKIN DEFECTS (MLS), A DOMINANT MALE-LETHAL DISORDER  
 CC CHARACTERIZED BY EYE, SKIN AND CENTRAL NERVOUS SYSTEM (CNS)  
 CC MALFORMATIONS.  
 CC -1- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.  
 CC  
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 CC  
 CC EMBL; AF117067; AAF43261.1;  
 CC EMBL; AF177663; AAD53166.1;  
 CC EMBL; AF177665; AAD53087.1;  
 CC EMBL; AF012272; AAC98539.2;  
 CC EMBL; AF022212; AAC98540.2;  
 CC HSP; Q07960; IRGP.  
 CC Genew; HGNC:676; ARHGAP6.  
 CC MIM; 300118;  
 CC MIM; 309801;  
 CC InterPro: IPR000198; RhoGAP.  
 CC Pfam: PF00620; RhoGAP: 1.  
 CC SMART; SM00324; RhoGAP: 1.  
 CC Alternative splicing: GTPase activation; SH3-binding.  
 CC SITE 342 352 RHO-GAP.  
 CC DOMAIN 411 584 MISSING (IN ISOFORM 4 AND ISOFORM 5).  
 CC VARSPLIC 196 196 E -> ELEGIDLIILGTRPPMNSDTHNFDTATLRMO  
 CC VARSPLIC 637 658 (IN ISOFORM 2).  
 CC VARSPLIC 659 974 SPMLSEVSVSGRHSSTDS -> TSSVLPAAYQACPOY  
 CC VARSPLIC 726 765 PAMSTFP (IN ISOFORM 2).  
 CC VARSPLIC 766 974 DLSEPFDTGTHSTLKSQKPGMTGSSGDIFESSLR  
 CC CONFLICT 231 231 -> GMSLASREWPQATLLILHVMCAIGALTFSSSLYLM  
 CC CONFLICT 231 231 FL (IN ISOFORM 1 AND ISOFORM 5).  
 CC CONFLICT 231 231 P -> A (IN REF. 2; AAD53166).  
 CC SEQUENCE 974 AA; -105973 MW; F7D63AE78720DB25 CRC64;  
 Query Match 2.5%; Score 100.5; DB 1; Length 974;  
 Best Local Similarity 18.6%; Pred. NO. 9.9; Indels 385; Gaps 46;  
 Matches 178; Conservative 99; Mismatches 294;  
 QY 27 AGSGRARGADTCGRNKA-----AARPLCVANEGVGPASRN----- 64  
 Db 51 AGAGSGARGA-TAG-RLYSPSLPAESLGRPLASSRGPPTATRLPPPGPLCSSTSTPT 108  
 QY 65 -----SCLNITFKYDNCITTYLNVG-----KHVIADQNTITTSQYACHQDVAVTILWS 113  
 Db 109 PQKSPSG-----SFHFD-----YEVPLGRGLKSKMADLPVSLAGPASSRASSILCSGG 160  
 QY 114 PGALGIEFLKGRVILEELKSGROCOOLILKPKOLNSFFKRTGMESSQFLNMFATDY 173  
 Db 161 GPGNGI-----FASPRWLQKQFQSPD-----SRGHPTVWVKSGDF 199  
 QY 174 F-----VKVPPFSPKNSYH-----PEFFETRACOLLQ-----PDNLACKPFWK 215  
 Db 200 TWNMSGSRVLSVPSQISLELRLQVETPQOQDCQLSCQITIPKQOKRK---K 256  
 QY 216 PRLNLSHGSDMQVSDFDHPAHNFGFRFFYL-----HYKLKE----- 254  
 Db 257 SURKELDSLAGEKNDKEFIPOAFGMPLSQVIANDRAYKLAKQDLQDEQKADSFVSL 316

QY	255	PFKRTCKQE-----QTETISCLQNYSFG-----DYIEELVDD 289
DB	317	PGNKRONKSSSSSSSSSTSEPN-----ESTSPWPEAPARRRRGAMSVDSITDLDN 373
QY	290	TNTRYKVMH-----YALKPVHSWAGPIRAVAITVPLVVISAFATL- 330
DB	374	QSRLEALQSLPAEAQSKKAKDKKLSLNIYR-----QVRLVDSCQHLE 422
QY	331	FTVMCKRKQOENITSHLOE-----ESSESTYTAALPERLRPRKPVFL- 374
DB	423	KHGLQTGVIFVGSKKRVQLREDFQIGDYSLEESVHDVALLKEFLDMAPLPT 482
QY	375	---CYSS-----KQONENNVVQCFATLDFQCCGVALQWE-----DPSLCREG 417
DB	483	RELTAIYNILLLEPEQIGTQLILYILPP---CRDYLHRLQLFSLVARADNISQG 541
QY	418	Q-----REWVIO-----KHESQITVIVCSKGMKVFVK 446
DB	542	QETVGNKTSLSNLATFQNLHKKQSSDKQESVOSSARAESTALIAVQKMI----- 595
QY	447	KYHKHGGGSGKGELEFVAVSAEKL-----RQAKQSSAAL----- 486
DB	596	ENYE-----ALFVPPDLQHEVLISLETDPDVYLLERKASOSSPDMLQSE 644
QY	487	-----SKFIAYFDYSCED-----VPGILD 507
DB	645	VSVGSGRHSSTDSKASGSDISPTDNNSPVLSRLLAQEDAAPGSGSEKLYVPQCFM 704
QY	508	L-----STKYRLMDLPLQCSHL-----BSR-DHGLQEPQOUTGCRSRNFFRS 750
DB	705	LVGHLSSKSRSSPCBRLGRLDSEPPDFQWHTSLKSGSKDGM---TGSSGDIFES 761
QY	551	KSGSLSVATCNMHQFIDEREPPWFQFVPPHPPPLRYREPVLEKFDGSLVLDVCKPG 610
DB	762	8-----SLRAGPCSLSG-SLSPNPPWQSGP-----AELDS-----792
QY	611	PESDFCLKYENAVLGCATPADSQSHQGLDQCEARPALDQSAALQPLLHTVKAGS98 670
DB	793	-DTQAGARRQAA-----APA-----TGRAPRAYSACSTPHVQVQAKAERT 834
QY	671	DMPRD-----SGLYDSVSPSELSPLMEGLSLDTQETSSITESVSSSGLEERPP 722
DB	835	ARSEQIYILSGANDLS-----ESELVAGLSRAIPQCR-----PHGSGRODKRPP 881
RESULT 13		
Z151_MOUSE		
ID	Z151_MOUSE	STANDARD; PRT; 794 AA.
AC	Q60821; Q60699;	
DT	15-JUL-1998 (Rel. 36, Created)	
DT	15-JUL-1998 (Rel. 36, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Zinc finger protein 151 (Polymavirus late initiator promoter binding protein) (LP-1) (zinc finger protein z13).	
GN	ZNF151 OR ZFP100.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.	
NCBI	TaxID:10090;	
RP	SEQUENCE FROM N.A.	
RA	Rapp L, Carmichael G.G.;	
RA	Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.	
RP	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-CBA; TISSUE=Kidney;	
RA	MEDLINE=96003919; PubMed=7575457;	
RT	Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;	
RT	An unusual arrangement of 13 zinc fingers in the vertebrate gene	
RT	z13.;	
CC	Biochem. J. 311:219-224(1995).	
CC	-1- FUNCTION: MAY FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT	

Db 207 AAACALSESSEDEMEVPSKNG--EDQEEGAGPATVKEBGNH-LDNGEPPERNESA 263  
 QY 678 YDSSVPSSESLP---LAEGLSTQDTETSLATESVSSSGIGEE 719  
 Db 264 GTDS--QQLGEGQNLASGYGDTESKAYGSIHKCEDGKE 305

## RESULT 14

ZFY2 MOUSE STANDARD; PRT; 783 AA.  
 AC P20662;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE zinc finger Y-chromosomal protein 2  
 GN ZFY2-OR. ZFY-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-89168416; PubMed-2493989;  
 RA Mardon G., Page D.C.;  
 RT "The sex-determining region of the mouse Y chromosome encodes a  
 protein with a highly acidic domain and 13 zinc fingers."  
 RL Cell 56:765-770(1989).  
 CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC  
 FINGER PROTEINS. ZFY/ZFY SUBFAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M24401; AAA56845.1;  
 DR PIR; A31491; A31491.  
 DR HSSP; P08048; 5ZNF.  
 DR MGD; MGI:992113; Zfy2.  
 DR InterPro; IPR000822; znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2; 13.  
 DR PRINTS; PR00048; ZINC\_FINGER.  
 DR ProDom; PD000003; znf\_C2H2; 1.  
 DR SMART; SM00355; znf\_C2H2; 13.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 10.  
 KW Transcription regulation; Activator; zinc-finger; Metal-binding;  
 KW DNA-binding; Repeat; Nuclear protein; LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 372 382  
 FT ZINC FINGERS.  
 FT ZNF\_FING 403 777  
 FT ZNF\_FING 403 425  
 FT ZNF\_FING 434 456  
 FT ZNF\_FING 466 488  
 FT ZNF\_FING 497 520  
 FT ZNF\_FING 526 548  
 FT ZNF\_FING 554 577  
 FT ZNF\_FING 583 605  
 FT ZNF\_FING 611 634  
 FT ZNF\_FING 640 662  
 FT ZNF\_FING 668 691  
 FT ZNF\_FING 697 719  
 FT ZNF\_FING 725 748  
 FT ZNF\_FING 754 777  
 SQ SEQUENCE 783 AA; 88856 MW; 1722D1C23F019D88 CRC64;

Query Match 2.5%; Score 99; DB 1; Length 783;  
 Best Local Similarity 19.2%; Fred. No. 9.6;

Matches 117; Conservative 74; Mismatches 207; Indels 210; Gaps 34;  
 QY 71 PFYONCTTTLNPGVGHVLAADANITISQYACHQVAVTILWSPGALGTEFLKGRVILE 130  
 Db 339 TAANDNSDEI---EVQNTASAMLHDSG-----GLD-----RVFKQ 374  
 QY 131 ELKS---EGRCQQILNDPKQLNSFKKTKGESOP---FLNMFFEDYFVVKVPPFSIK 184  
 Db 375 KSKKKRPESKQSAIFVAPDQGT-----LRVYPCMGCKKFKKFLK---RHIK 423  
 QY 185 NESYHPPFFTRACDLLOPDNLACKPFWKPRNLNISOHGSMDQVFSDBAPENGRFF 244  
 Db 424 N-----HPEYLANKY---HCTEDYSTNKKIS----- 448  
 QY 245 YLYKLKHGEPFKKTKCOBOTVETTSCLLOWNSPDYIIELVDTNTWTKVMYALKPV 304  
 Db 449 LHNEMESH---KLTIKTEKTECDDC-RKNLSHA-----GILCTHKTMEY 490  
 QY 305 BSPWAGPIRAVAITVPLVI---SAPATLEF---VMCKKQENIYSHLDESSESSTY 357  
 Db 491-----KGVNCKCKPCDYETABOTLHLLHLLVHKK-----FFHICGCGGRFRH 537  
 QY 358 TAALPRE-RLRPRKVFELC---YSSKDCQN---HNVVQCFAFYLDQFGCEVALDWE 409  
 Db 538 PSALKKHIRVHTGKPYECYCEYKSSADSSNLATHIKSHKEIPLA---CDICL---L 590  
 QY 410 DFSLCRSGQREWI---QKIHESOFILVVCCKGMKYFVDKRNKTHKGGGSGKGEFLV 466  
 Db 591 NFSDTKEAQOHAHVHQSRTHQ-----CS-----HCNKKSSNSDLKRIILSV 633  
 QY 467 AVSIAEKLQKQAGS---SSAALSXFIAYFYDYS-----CEGDVPG-----ILDLSK 511  
 Db 634 ETKAYPHKCMCKSGFHPSELAKKHVATHSKKMGHCRCDFNSDPDFLLSHILLSATK 693  
 QY 512 YLMDNLPOLCSLHLSRDEGLQEPQHTQSGSRNRYFKSKRSLYVATCMHQFIDEEP 571  
 Db 694-----NYPFKKCKCK-----EPQOCELOTHMTHSHSRKVTQ---CEYCEYSTDA 737  
 QY 572 DWFKQVPPHPPPLKRPVLEKFDPSGLVNDVMCKGPESDPCLKLVAAVLGATGAD 631  
 Db 738 SGFKRHVISHTKDPHR-----CDFCKK-----GFRPSE 768  
 QY 632 -SQESQOR 638  
 Db 769 KNOHMRH 776

## RESULT 15

PSU1 YEAST STANDARD; PRT; 970 AA.  
 AC P53550;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE mRNA deapping protein 2 (PSU1 protein).  
 GN DCP2 OR PSU1-OR YNL118C OR N1917.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID-4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-D273-10B;  
 RA Tzagoloff A.A.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-9745296; PubMed-9090055;  
 RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,  
 RA Pallavicini A., Lanfranchi G., Valle G.;  
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of  
 RT Saccharomyces cerevisiae reveals an unusually high number of  
 RT overlapping open reading frames.";





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JANUARY 10, 1901  
REPORT  
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ADMINISTRATION  
OF THE  
OFFICE  
DURING THE  
YEAR  
1900  
BY  
JAMES C. HARRIS  
ATTORNEY GENERAL

GenCore version: 5.1.4.p5.4578  
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OM protein - protein search, using sw.model

Run on: May 19, 2003, 09:14:29 / Search time 99.0725 Seconds  
(Without alignments)  
2626.495 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1.MAPVLQQLSVFFTVNACLNG.....CKADLCGRSYTDELHVAAPL 753

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580.seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 04

Maximum Match 1004

Listing first 45 summaries

Database:

- 1: sp.archaea.\*
- 2: sp.bacteria.\*
- 3: sp.fungi.\*
- 4: sp.human.\*
- 5: sp.invertebrate.\*
- 6: sp.mammal.\*
- 7: sp.mhc.\*
- 8: sp.organelle.\*
- 9: sp.phage.\*
- 10: sp.plant.\*
- 11: sp.rodent.\*
- 12: sp.virus.\*
- 13: sp.vertibrate.\*
- 14: sp.unclassified.\*
- 15: sp.rvirus.\*
- 16: sp.bacteriap.\*
- 17: sp.archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3005	74.9	564	Q9UFA0	Q9UFA0 homo sapien
2	2616.5	65.2	582	11 Q8R5J8	Q8R5J8 mus musculus
3	1961	48.9	745	13 Q8OHJ9	Q8OHJ9 brachydanio
4	1952	48.6	745	13 Q8OHJ6	Q8OHJ6 brachydanio
5	170.5	4.2	846	5 Q9A6A	Q9A6A caenorhabdli
6	117.5	2.9	562	4 Q99755	Q99755 homo sapien
7	117	2.9	757	3 Q13399	Q13399 uscllago ma
8	117	2.9	917	10 Q81789	Q81789 arabidopsis
9	117	2.9	2846	10 Q84634	Q84634 arabidopsis
10	116.5	2.9	901	16 Q9KE04	Q9KE04 bacillus ha
11	115.5	2.9	938	11 Q60669	Q60669 mus musculus
12	112.5	2.8	549	4 Q99754	Q99754 homo sapien
13	111.5	2.8	348	4 Q9H460	Q9H460 homo sapien
14	111.5	2.8	370	4 Q96KN9	Q96KN9 homo sapien
15	110	2.7	428	4 Q9NTU6	Q9NTU6 homo sapien
16	108.5	2.7	3788	11 Q942X9	Q942X9 rattus norv

17	108	2.7	903	5 Q95WA7	Q95WA7 bulla Gould
18	108	2.7	1058	10 Q9AV10	Q9AV10 cryza sativ
19	108	2.7	1962	11 Q9WUF3	Q9WUF3 mus musculu
20	107.5	2.7	3942	11 Q88732	Q88732 mus musculu
21	107	2.7	1322	11 Q9QZP6	Q9QZP6 mus musculu
22	107	2.7	1545	11 Q8VBS6	Q8VBS6 mus musculu
23	107	2.7	3788	11 P97412	P97412 mus musculu
24	106.5	2.7	638	10 Q9LQF8	Q9LQF8 arabidopsis
25	106.5	2.7	1907	4 Q15017	Q15017 homo sapien
26	106	2.6	549	5 Q19655	Q19655 caenorhabdli
27	106	2.6	593	11 Q99PV2	Q99PV2 rattus norv
28	106	2.6	1448	16 Q8VWJ8	Q8VWJ8 anabaena sp
29	106	2.6	1516	4 Q9C0D2	Q9C0D2 homo sapien
30	105.5	2.6	901	5 Q24573	Q24573 drosophila
31	105	2.6	1545	5 Q9BHW7	Q9BHW7 leishmania
32	105	2.6	1571	11 Q54978	Q54978 mus musculu
33	105	2.6	2031	5 Q9N918	Q9N918 leishmania
34	104.5	2.6	707	4 Q96SK7	Q96SK7 homo sapien
35	104.5	2.6	806	5 Q3VOK5	Q3VOK5 drosophila
36	104.5	2.6	924	10 Q9FVDS	Q9FVDS arabidopsis
37	103.5	2.6	625	10 Q9FMD7	Q9FMD7 arabidopsis
38	103.5	2.6	1289	11 Q9WTR2	Q9WTR2 mus musculu
39	103.5	2.6	1306	2 Q9L8Z1	Q9L8Z1 enterococcu
40	103	2.6	1156	5 Q967X9	Q967X9 tribolium c
41	103	2.6	1428	5 Q9VU03	Q9VU03 drosophila
42	102	2.5	1654	5 Q9VC36	Q9VC36 drosophila
43	102	2.5	4169	4 Q8TCU4	Q8TCU4 homo sapien
44	101.5	2.5	341	6 Q9NOB3	Q9NOB3 macaca fasc
45	101.5	2.5	1639	3 Q9P707	Q9P707 schizosacch

#### ALIGNMENTS

##### RESULT 1

Q9UFA0 PRELIMINARY; PRT; 564 AA.  
AC Q9UFA0  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE Hypothetical 63.1 kDa protein (Fragment).  
GN DKFZP434M1928  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_taxid=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=TESTIS;  
RC Bloembergen H., Boecher M., Brandt P., Newes H.W., Gassenhuber J.,  
RA Wienann S.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL133097; CAB61408.1;  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E88C CRC64;

Query Match 74.9%; Score 3005; DB 4; Length 564;  
Best Local Similarity 99.8%; Pred. No. 1.2e-266;  
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	190	HPFFFRACDILLQDNLACKPTKPKRNINISQGSQMSQVSPDHPHNGFRFFLYHK	249
DB	1	HPFFFRACDILLQDNLACKPTKPKRNINISQGSQMSQVSPDHPHNGFRFFLYHK	60
QY	250	LKHGSPFKRTKQEQTTTSCLLQNVSPGDYIIELVDDTNTTKRYMHTALPKVHSPWA	309
DB	61	LKHGSPFKRTKQEQTTTSCLLQNVSPGDYIIELVDDTNTTKRYMHTALPKVHSPWA	120
QY	310	GPTRAVAITVPLVVSATFATLFTVMCKKQENITSHLDESSSSSTTTAALPRELRPR	369
DB	121	GPTRAVAITVPLVVSATFATLFTVMCKKQENITSHLDESSSSSTTTAALPRELRPR	180

QY 370 PKYFLCTSSKCGONHNNVOCFAIFLQDPCGCEVALDNEFSLCBREGQREWIQKHES 429  
 DB 181 PKYFLCTSSKCGONHNNVOCFAIFLQDPCGCEVALDNEFSLCBREGQREWIQKHES 240  
 QY 430 QFIIVVCSGKMYFVOKNTKHKGGGSGGKGLFLVAVSAIAELKRAKQSSAALSXP 489  
 DB 241 QFIIVVCSGKMYFVOKNTKHKGGGSGGKGLFLVAVSAIAELKRAKQSSAALSXP 300  
 QY 490 IAYFDYCEBQDVFGIIDLSTKYLMDNLPLQCSHLSRDHQLQEPGQRTGSRNRYR 549  
 DB 301 IAYFDYCEBQDVFGIIDLSTKYLMDNLPLQCSHLSRDHQLQEPGQRTGSRNRYR 360  
 QY 550 SKSGRSLYVACNMHOFIDEPDWFKEQFVFPHPPLRYREPYLEKFDGSLVNDVNCXP 609  
 DB 361 SKSGRSLYVACNMHOFIDEPDWFKEQFVFPHPPLRYREPYLEKFDGSLVNDVNCXP 420  
 QY 610 GPESDCLAVEAALVAGATPADSOHESQBGGLQDGEARALDGSANALQPLHTYKAGSP 669  
 DB 421 GPESDCLAVEAALVAGATPADSOHESQBGGLQDGEARALDGSANALQPLHTYKAGSP 480  
 QY 670 SDMPRSGIYDSSVPSSLSLPLMBGLSTDOTETSSLSLTSVSSSSGLGEEPPALPSKLL 729  
 DB 481 SDMPRSGIYDSSVPSSLSLPLMBGLSTDOTETSSLSLTSVSSSSGLGEEPPALPSKLL 540  
 QY 730 SSGCKADIGCRSTYDELHVAAPL 753  
 DB 541 SSGCKADIGCRSTYDELHVAAPL 564

## RESULT 2

ID Q8R5J8 PRELIMINARY; PRT; 582 AA.  
 AC Q8R5J8;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DE Similar expression to FGF protein (fragment).  
 GN Sef.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21824237; PubMed-11802165;  
 RA Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;  
 RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF  
 signalling.";  
 RL Nat. Cell Biol. 4:170-174(2002).  
 DR ENBL; AF424804; AAL79530.1;  
 FT NON TER 1  
 SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 65.28; Score 2616.5; DB 11; Length 582;  
 Best Local Similarity 84.66; Pred. No. 5.6e-231;  
 Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

QY 171 TDYFKVVPFSSIKNESNYHFFFTFRACDLLOPNLACKPFWKPNLNISQBGSDMOV 230  
 DB 1 TDYFKVVPFSSIKNESNYHFFFTFRACDLLOPNLACKPFWKPNLNISQBGSDMOV 60  
 QY 231 SFDHAPNFGREFLYHKLKHEGPFKRTCKOQTETTSCLQVSPGDIYIELVDOT 290  
 DB 61 SFDHAPNFGREFLYHKLKHEGPFKRTCKOQTETTSCLQVSPGDIYIELVDOT 120  
 QY 291 NTRKVMYALQVHSPWAGPIRAVAITVPLWISAPATLFTVMCKKQENIYSHLDEE 350  
 DB 121 NTRKVMYALQVHSPWAGPIRAVAITVPLWISAPATLFTVMCKKQENIYSHLDEE 180  
 QY 351 SSESSTYAAALPRRLRPRPKVFLCYSSKQGNHNNVOCFAIFLQDPCGCEVALDNEF 410  
 DB 181 SPESSTYAAALPRRLRPRPKVFLCYSSKQGNHNNVOCFAIFLQDPCGCEVALDNEF 240

QY 411 FSLCBREGQREWIQKHESQFIIVVCSGKMYFVOKNTKHKGGGSGGKGLFLVAVSA 470  
 DB 241 FSLCBREGQREWIQKHESQFIIVVCSGKMYFVOKNTKHKGGGSGGKGLFLVAVSA 300  
 QY 471 IAEKRAKQSSAALSXP IAYFDYCEBQDVFGIIDLSTKYLMDNLPLQCSHLSRDH 530  
 DB 301 IAEKRAKQSSAALSXP IAYFDYCEBQDVFGIIDLSTKYLMDNLPLQCSHLSRDH 357  
 QY 531 GLQEP-GQRTGSRNRYRFSKSGSLVACNMHOFIDEPDWFKEQFVFPHPPLRYR 589  
 DB 358 GLQEP-GQRTGSRNRYRFSKSGSLVACNMHOFIDEPDWFKEQFVFPHPPLRYR 417  
 QY 590 EPLVLEKFDGSLVNDVNCXPGEPSDFCLKVEAALVAGATPADSOB-ESQBGGLQDGEA 647  
 DB 418 EPLVLEKFDGSLVNDVNCXPGEPSDFCLKVEAALVAGATPADSOB-ESQBGGLQDGEA 477  
 QY 648 RALDGSANALQPLHTYKAGSPSDMPRSGIYDSSVPSSLSLPLMBGLSTDOTETSSLT 707  
 DB 478 QPSDCLAVEAALVAGATPADSOHESQBGGLQDGEARALDGSANALQPLHTYKAGSP 537  
 QY 708 ESYSSSSGLGEEPPALPSKLLSSGCKADIGCRSTYDELHVAAPL 753  
 DB 538 ESYSSSSGLGEEPPALPSKLLSSGCKADIGCRSTYDELHVAAPL 582

## RESULT 3

ID Q8QJ9 PRELIMINARY; PRT; 745 AA.  
 AC Q8QJ9;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DE Similar expression to FGF protein (fragment).  
 GN Sef.  
 OS brachydanto rerio (zebrafish) (zebra danio).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 CC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21824236; PubMed-11802164;  
 RA Tsang M., Friesel R., Kudoh T., Dawid I.;  
 RT "Identification of Sef, a novel modulator of FGF signalling.";  
 RL Nat. Cell Biol. 4:165-169(2002).  
 DR ENBL; AF364103; AAL76112.1;  
 SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DDB4 CRC64;

Query Match 48.93; Score 1961; DB 13; Length 745;  
 Best Local Similarity 51.48; Pred. No. 1.1e-170;  
 Matches 390; Conservative 114; Mismatches 197; Indels 58; Gaps 10;

QY 1 MAPWQLCVFVFNACLSQSLAVAGGSGRARGADTCGWRKAKAAARPLCVANRGVGP 60  
 DB 7 LAHFFMASCLFLCTASVNG-----GKRGNSDKCSYK-----QGTQT 43  
 QY 61 ASRNSGL--YNTFKYDNCTTYLNPVGRHVIADAQNTISYACHDQVAVTILWSPGALG 118  
 DB 44 SMDGSKLGVTFRDYDNCVYNNPLGRHAEVNNITFSLSCDSQAAYVWVWMAPIG 103  
 QY 119 IEFLGPFVILELSEGGKOCOLLKDKPLKNSFKGKESOPFLNNKFEDYFKVY 178  
 DB 104 IEHVGAFVILELSEGGKOCOLLKDKPLKNSFKGKESOPFLNNKFEDYFKVY 163  
 QY 179 PPTSKNESNYHFFFTFRACDLLOPNLACKPFWKPNLNISQBGSDMOVSDHAPIN 238  
 DB 164 PPTSKNESNYHFFFTFRACDLLOPNLACKPFWKPNLNISQBGSDMOVSDHAPIN 223  
 QY 239 FGFREFLYHKLKHEGPFKRTCKOQTETTSCLQVSPGDIYIELVDOTTTTKVH 298  
 DB 224 FGFREFLYHKLKHEGPFKRTCKOQTETTSCLQVSPGDIYIELVDOTTTTKVH 283

QY 299 YALAFVSHVWAGPITRAVAVTIVPLVLSAFATLFTVMCKKQENIYSHLDESSSTYT 358  
 DB 284 YHVSQVSHVWAGPITRAVAVTIVPLVLSAFATLFTVMCKKQENIYSHLDESSSTYT 343  
 QY 359 AALPRELPRPRKPVLCYSSKQONHNTVQCFAYFLQDFCGCEVALDQWDFSLCBEGQ 418  
 DB 344 TALSDRPRPRKPVLCYSSKQONHNTVQCFAYFLQDFCGCEVALDQWDFSLCBEGQ 403  
 QY 419 RENVIOKHESOFIIVVCKGMYFYVDKKNYKHGGGR-----GSGKGEFLVA 467  
 DB 404 MSWLSRRIDEAFHITVCSKGLHFVFKHRKRGKATSKENRPSASDSSSSRDLEIVA 463  
 QY 468 VSAIAEKLQAKQSSAALSFAVTFDYSCGDPVGLDLSKYRLMDNLPOLCSHLRS 527  
 DB 464 SAILSEKLEVBQKSS-DLSRPMVTFDYSHETDPTSLAPKFLMDLPOLFAHLS 522  
 QY 528 RDHGLQEPQHTROGSRNTFRSKGSLYVAICNMQPFDDEPQWFKQVPPHPPPLR 587  
 DB 523 ROLSLDREPPQPNVSKNTFCSKGSLYVAICNMQPFDDEPQWFKQVPPHPPPLR 579  
 QY 588 YREPVLKEDSLVNDVCKPQSPDCLKVEAVL-----GATPADSQHESQHG 640  
 DB 580 NKRTIPKVDGSLVNDVCKPQSPDCLKVEAVL-----GATPADSQHESQHG 638  
 QY 641 LDQGEARPALDGSAAQLOPLHTVKGASPMRDSGYDSSVPSSELSPLMBGLSTQ 700  
 DB 639 SSOD-----AGSCRPLVHTDGSAPPMRDSGYDSSVPSSELSPLMBGLSTQ 689  
 QY 701 TETSSLTSSVSSSGLGDEPPALPALKLLSSGS-CKADL 738  
 DB 690 ADNSSLADSVSSSGLGDEPPALPALKLLSSGS-CKADL 728

RESULT 4  
 Q80R76 PRELIMINARY; PRT: 745 AA.  
 ID Q80R76  
 AC Q80R76  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Y64G10A.6 protein.  
 GN Y64G10A.6  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21824237; PubMed-11802165;  
 RA Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;  
 RT "Self is a feedback-induced antagonist of Ras/MAPK-mediated FGF  
 RT signaling";  
 RL Nat. Cell Biol. 4:170-174(2002).  
 RP SEQUENCE FROM N.A.  
 RA Furthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF401232; AAL78817.1;  
 SQ SEQUENCE 745 AA; 83437 MW; 759B9EDCC08A4652 CRC64;

Query Match 48.6%; Score 1952; DB 13; Length 745;  
 Best Local Similarity 51.1%; Pred. No. 7, 6e-170;  
 Matches 388; Conservative 116; Mismatches 197; Indels 58; Gaps 10;

QY 1 MAPK1QCSVFTVYVACNLSQSLAVAGSGRAGADTCGRWKAARPRVCYANEGVGP 60  
 DB 7 LAUFFHASCILCYTASVNG-----GKGNKDKCSYK-----QGTQT 43  
 QY 61 ASRNSGL--YNTFKYDNCYTYLNPVGRHVATADQNTISQYACHQDVAVTILMSPCALG 118  
 DB 44 SSMDEGARKLVGTRYDNCVSNNSPLGKAHIEVNNISFSLSCDSQAQVAVVWNASPLG 103

QY 119 IETLKFVRLLEKASBGRCCQQLILKDPKQLNSPFTQCSOPPLMKKETDTYFKVV 178  
 DB 104 IETLKFVRLLEKASBGRCCQQLILKDPKQLNSPFTQCSOPPLMKKETDTYFKVV 163  
 QY 179 PPSIKNESNHPFFTRACDILLOPDLACKPFWKPRNLNISQSGDMQVSDHAPHN 238  
 DB 164 PPSIKNESNHPFFTRACDILLOPDLACKPFWKPRNLNISQSGDMQVSDHAPHN 223  
 QY 239 FGRFFTYLKLKHEGPFKAKTKQBTETTSCLLQNVSPGDIYIELVDVDTNTRKVMH 298  
 DB 224 FGRFFTYLKLKHEGPFKAKTKQBTETTSCLLQNVSPGDIYIELVDVDTNTRKVMH 283  
 QY 299 YALPVPESHVWAGPITRAVAVTIVPLVLSAFATLFTVMCKKQENIYSHLDESSSTYT 358  
 DB 284 YHVSQVSHVWAGPITRAVAVTIVPLVLSAFATLFTVMCKKQENIYSHLDESSSTYT 343  
 QY 359 AALPRELPRPRKPVLCYSSKQONHNTVQCFAYFLQDFCGCEVALDQWDFSLCBEGQ 418  
 DB 344 TALSDRPRPRKPVLCYSSKQONHNTVQCFAYFLQDFCGCEVALDQWDFSLCBEGQ 403  
 QY 419 RENVIOKHESOFIIVVCKGMYFYVDKKNYKHGGGR-----GSGKGEFLVA 467  
 DB 404 MSWLSRRIDEAFHITVCSKGLHFVFKHRKRGKATSKENRPSASDSSSSRDLEIVA 463  
 QY 468 VSAIAEKLQAKQSSAALSFAVTFDYSCGDPVGLDLSKYRLMDNLPOLCSHLRS 527  
 DB 464 SAILSEKLEVBQKSS-DLSRPMVTFDYSHETDPTSLAPKFLMDLPOLFAHLS 522  
 QY 528 RDHGLQEPQHTROGSRNTFRSKGSLYVAICNMQPFDDEPQWFKQVPPHPPPLR 587  
 DB 523 ROLSLDREPPQPNVSKNTFCSKGSLYVAICNMQPFDDEPQWFKQVPPHPPPLR 579  
 QY 588 YREPVLKEDSLVNDVCKPQSPDCLKVEAVL-----GATPADSQHESQHG 640  
 DB 580 NKRTIPKVDGSLVNDVCKPQSPDCLKVEAVL-----GATPADSQHESQHG 638  
 QY 641 LDQGEARPALDGSAAQLOPLHTVKGASPMRDSGYDSSVPSSELSPLMBGLSTQ 700  
 DB 639 SSOD-----AGSCRPLVHTDGSAPPMRDSGYDSSVPSSELSPLMBGLSTQ 689  
 QY 701 TETSSLTSSVSSSGLGDEPPALPALKLLSSGS-CKADL 738  
 DB 690 ADNSSLADSVSSSGLGDEPPALPALKLLSSGS-CKADL 728

RESULT 5  
 Q80R64 PRELIMINARY; PRT: 846 AA.  
 ID Q80R64  
 AC Q80R64  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Y64G10A.6 protein.  
 GN Y64G10A.6  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99059613; PubMed-9851916;  
 RA none;  
 RA Ainscough R.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99059613; PubMed-9851916;  
 RA none;  
 RA "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology";  
 RT Science 282:2012-2018(1998).  
 DR EMBL; AL110498; CAB54470.1;  
 SQ SEQUENCE 846 AA; 94852 MW; 613AEF55EB889BA4 CRC64;

Query Match 4.2%; Score 170.5; DB 5; Length 846;

Best Local Similarity 21.4%, Pred. No. 2.5e-06;  
Matches 141, Conservative 82, Mismatches 225, Indels 211, Gaps 37;

QY 99 QYACHDQVAVTILWSPGALGIEFLKGFVLELSEKGGCCOOLILKDPOLANSFKRTG 158  
Db 294 QY-CFEZEVLDDSS--GIVMGSALITKDELATE-----IINGRVPQGER-----338

QY 159 MESQPLANKFETDYFVKVPPPSIKNESYHFFFRACDQLLQDNLAC-KFKNR 217  
Db 339 ---NFTDIELODILTPSVIPESAHQ-----GRC-LCVTENGSCSLADMKPV 382

QY 218 NLIISQSGDMQVSDFAHPNFGFRFFLYHLKHEGPKFKTKQQTETTSCLLQNV 277  
Db 383 KLT-----RIKPPATSN-----QTESDCKAEKDKREDTWT-----415

QY 278 SPEDYIIEVDVNTTRKVMH-YALKPVHSPWAGPRAVATVPLWISAPATL--FTVM 334  
Db 416 -----WHTYA-----ITGGAIILAILFSLVCAGLCKYKF 445

QY 335 CRKQENITSHLDESSSTTTAALPRERLRPRKPVLCYSSKDGQNMNVVOCFAF 394  
Db 446 NKKEASNI--HLLENPAFS-HSGSIP-LILQISVLIVY-SHDSAQEAAVLAPAE 500

QY 395 LQDCCGEVALDWEDFSCRGQREWVQIKHESOFIIVCSGKMYFVDDKNYKHGG 454  
Db 501 LNDVFNLAHLVDWEDQI-ENRAEYINSSIVRANKYIINSIG-AIF--RVTFRHOR- 555

QY 455 GRGSGKGLFVAVSAIAEKLQAKOSSAALSFKTAVTFDYSCGDV--PGTLDLSKY 512  
Db 556 -----EPAIERITGRND-----VIFDMOCELALQHPCVISCHFSY 591

QY 513 -----RLMD-NLPOLCSHLRHGLOEPQOHTROGSRNRYFRSKRSILYAI 560  
Db 592 TNPKVVPPIINLLOYSIP--NSLMTWTALTQEPARPEQLAGFNQVFAR-----LQAAI 644

QY 561 CNKHOFIDEEDPMFK-----QVFPFPPPLAYR-----589  
Db 645 SRKLVIESDQWFENTHVRATRVSELEAHNIVL-PPSLVKVDEDAFCOMETLPI 703

QY 590 EYVLEKP-----DSGLVNDVMCKPESDFCLKVAANVLGATGPADQSIES 636  
Db 704 DELKFAKNDLEVDSEVDKLEEDVCAKGP-----IHVETPEVLEPAEPEE 758

QY 637 QHGGLDQGEARPALDGSAA-----LQPLL-HYKAGSPDMRDSGIYDSS-VPSSELS 689  
Db 759 ABED-BEEDDDVDSVEGATRIEELQLIVH-----KMNHDSGNLDSATYSGDSFS 809

RESULT 6  
Q99755 ID Q99755 PRELIMINARY; PRT; 562 AA.  
AC Q99755;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (BC 2.7.1.68).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RA MEDLINE-97115834; PubMed=8955136;  
RX Loijens J.C., Anderson R.A.;  
RT "Type I phosphatidylinositol-4-phosphate 5-kinases are distinct  
RT members of this novel lipid kinase family."  
EL J Biol Chem 271:32937-32943(1996).  
DR EMBL:U78576; AAC50911.1;  
DR InterPro: IPR002498; Pfam:  
DR SMART: PF01504; Pfam: 1.  
DR SMART: SM00330; Pfam: 1.  
KW Kinase; Transferase.

SO SEQUENCE 562 AA: 62633 MW: A8F7988EB73506A0 CRC64;  
Query Match 2.98%; Score 117.5; DB 4; Length 562;  
Best Local Similarity 18.1%; Pred. No. 0.098;  
Matches 133, Conservative 105, Mismatches 239, Indels 257, Gaps 35;

QY 53 VANGVGPASRNGSLYNTFYDNCIT-----YLPVGVKVIADQAQNTITISQACHDQV 106  
Db 1 MASASSPSS-SYGFSSFDPAVPSCITSSAAAGIKRPMASEVLEARDSDYISLV-----53

QY 107 AVTILSPGALGIEFLK-GFRVLEELKSGCCOOLILKDPOLANSFKRTGMSOPFL 165  
Db 54 -----PTASGMPKKIKHRSVDSGCTTYKATSSALKAGQGLGITHVVSLSLTKPER 106

QY 166 NKKEETDYFVKVPPPS-----IKNESYHFFFRACDQLLQDNLACPKFKNRINI 221  
Db 107 DVLQMDFTVYESIFRPSGSLNLTDAHYNDFKTYA-----143

QY 222 SOHGSMDQVSDFAHPNFGFRFFLYHLKHEGPKFKTKQQTETTSCLLQNV 320  
Db 144 -----PVAFRFRELIGRPDYLKSLCSPLIELSCSSGASGSLEY-VSSDDEFIKT 195

QY 261 CRQQTETTSCLLQNVSPGYIIEVDVNTTRKVMH-YALKPVHSPWAGPRAVATV 320  
Db 196 VOHKEAE-----FLQKLLPGTYM-----NLQN-----P 219

QY 321 LVVISAPATLFTVMCKKQ-----OENYISHLDESSSTTTAALPRERLRPR 370  
Db 220 RTLLPKFTGLYCVQAGGKNIRIVVANNLLPRSVKMHKIDKLGSTYKRRASOKEREKPLP 279

QY 371 NVFELCYSSKDGQNMNVVOCFAFLODF-CGCEVALDWEDFSCRGQREWVQI--KI 426  
Db 280 -----TFKD-----LDPLQIDPLGLDADMTN--ALCKTLQDCLVLQSFKI 320

QY 427 HESQFLLV-----CSGKMYFVDDKNYKHEGSGGKGLFVAVSAIAEKL 476  
Db 321 MDYSLIASIHNIDHQAEPLESEFQISVOTR-----RPAKALYSTAMESIOGAR 372

QY 477 Q-----AKOSSAALSFKTAVTFDYSCGDVPGILDSTYRLMDNLPOLC 522  
Db 373 RGGTNETDMMGGITFARNKGERLLTY-----GIIDILQSTRFVVKLEHSH 419

QY 523 SBL-BSRDH-GLQEPQOHTROGSRNRYFRSKRSILYAIQNMHQFIDEEDPMFKQFVP 580  
Db 420 KALYVHEDGTVSVHRPGFAERFOR-----FMCN-----TVFVK--IP 454

QY 581 FHPPLPLRYEPVLEKFDGLVNDVMCKPESDFCLKVAANVLGATGPADQSIESQHG 640  
Db 455 LKPSFK-----NFRSS-----SSFSRRAGSSGNCITYQPSVSG-----EHAQ-- 494

QY 641 LDQGEARPALDGSAAALPILFTYKAGSPDMRDSGIYD-----SSVPSSELSLMEGL 696  
Db 495 -----VTKAEVEFGVH--LGRPDVLQTPPLEEISEGSPIDPSFS-FLV-GE 539

QY 697 STDQTTETSSLTESV 710  
Db 540 TLQMLTSTTLEKL 553

RESULT 7  
O13399 ID O13399 PRELIMINARY; PRT; 757 AA.  
AC O13399;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Telomere-associated recQ-like helicase (Fragment).  
GN OTASRECQ.  
OS Ustilago maydis (Smut fungus).  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginaceae; Ustilago.  
OX NCBI\_TaxID=5270;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-PB2;  
RA Sanchez-Alonso P., Guzman P.;  
RT Organization of chromosome ends in *Ustilago maydis*: recQ-like  
ET helicase motifs at telomeric regions;  
RL GenBank: AF030885; AB95264.1;  
DR EMBL: AF030885; AB95264.1;  
DR InterPro: IPR001410; DEAD.  
DR Pfam: PF00270; DEAD; 1.  
DR SMART: SM00490; HELICASE\_C; 1.  
DR SMART: SM00490; HELICASE\_C; 1.  
DR ATP-binding; Helicase.  
FT NON\_TER  
SQ SEQUENCE 757 AA; 84382 MW; 1AE1E41443532A7 CRC64;  
Query Match 2.9%; Score 117; DB:3; Length 757;  
Best Local Similarity 20.3%; Pred. No. 0.17;  
Matches 111; Conservative 56; Mismatches 167; Indels 190; Gaps 27;  
QY 268 ETTSCLLQWSPGDIYELVDOTNTKRVHYALAPVSPWAGPIRIV---AIVPL-- 321  
DB 77 ETTIILPTVALRANLAKLVN---IRHVQP-GSKAAPVIVSTEAATLAFKE 131  
QY 322 -----VYSAPATLFTVCKKKQENIYSHLDESSSTYTAALP----- 362  
DB 132 YANRLLQOOLDRIVDECHLTARSTYRSMOLAWHVRVETQTVMLTATLPPIFEA 191  
QY 363 ---RERLRPRKVF-----LCYSSKDGONHNVVOCF-AVFLDFGCGEVALDWEF 411  
DB 192 FISHNKLTKPLIVRESTNRSNICTSVTAERMSGNTCYDAVRVD--ECRAFTDM-- 246  
QY 412 SLCRSGRENVQIKIESOPIIVVCSKGMKVFYDK-----KNKKGGRGS----- 458  
DB 247 -----NQGED-----RIIVCTS--RELVARLAEMLCAYSSSEADKAIIQ 290  
QY 459 -----KGLEFLVAVSAIAEKLQAKQSSAALSFKTAVFYDCEGVPGIL--DLSTKY 512  
DB 291 DMWCKGSPVIVATSA-----LGVGFDPYHVRVIBLLGPDLALDF 331  
QY 513 -----RLADNLQCLSHLSRDLQEPQGHTRQGRSRYNFRS 550  
DB 332 SQSGRAGRGDMPAESILLAGPDLDRAP--ASGKASSAEKGVAPG---ADKEANQLYS 387  
QY 551 KSGRSLVAVICNHOFIDEPDFEKFQVFPFHPPLRYREPVEKFDGSLVNDVCKPG 610  
DB 388 RK-----YCLAGVLSQLDQSDW-----RWCMEGDQLCSVC 419  
QY 611 PESDFCLKVEAAVLGATGPDSQ---ESQHGGLDQDGEARPALDGSAAQLPILHTVRAG 667  
DB 420 PQHFF-----QARGPGQFHETAPAGDPSTQSRPSHMGSS--HPSNH----- 463  
QY 668 SPSPMDRSGIYDSSVPSSE--LSLPLMEGLSTQDTSETSLTESVSSS---SGLGEEPEPA 723  
DB 464 -----GSSPSPSGSSHPSHSGSSHPSHSGSSHPSHSGSSHPSHSGSSHPSHSGSS 757  
QY 724 LPSK 727  
DB 511 PPSE 514  
RESULT 8  
ID O81789 PRELIMINARY; PRT; 917 AA.  
AC O81789;  
DT 01-NOV-1998 (TEMBREL. 08, Created)  
DT 01-NOV-1998 (TEMBREL. 08, Last sequence update)  
DT 01-JUN-2002 (TEMBREL. 21, Last annotation update)  
DE Hypothetical 101.6 kDa protein.  
GN F8D20.70 OR A74G35560.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsals.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Koetter P., Hempel S., Entian K.-D., Hoheisel J., Jesse T.,  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).  
DR EMBL: AL031135; CAZ0026.1;  
DR EMBL: AL161587; CA880272.1;  
DR InterPro: IPR001680; WD40.  
DR Pfam: PF00400; WD40; 2.  
KW Hypothetical protein; Repeat; WD repeat.  
SQ SEQUENCE 917 AA; 101552 MW; 1809BDC42302C820 CRC64;  
Query Match 2.9%; Score 117; Length 917;  
Best Local Similarity 18.3%; Pred. No. 0.23;  
Matches 167; Conservative 130; Mismatches 296; Indels 320; Gaps 42;  
QY 19 NCSOLAVAGSGRAGADTCGRN--KAARER---LCVANECV----- 58  
DB 92 NGRSVSV---GYSNG-DILINSIPKSGCESPESAMICKLNGYSEKIPIASLKVY 145  
QY 59 --GPASR-----NSGLNITFKYDNCNTYLANPVGHV---IADQNI--TISQACHDQ 105  
DB 146 AEGKASRYVIGSSSSNQVLLNEQETETMILKGLRVSEPCADMEMIADVNEOSKIKQ 205  
QY 106 VAVTILNSPGALGI--EFLKGRVILEELASEROCQOILKDPQLNSFKARTQNESOP 163  
DB 206 DFLVFLKSGRVATDVMIEKYLIOQSCKSPSPKATVTVKLPFSSSITVGFFLNP 265  
QY 164 --FNMFETDY-----FVKVVEFPKIKNES--YHPFF-----FTRACDILLQPD 206  
DB 266 SHLLNLSD--DYAOLAKDAVPELFFHTVPKESRAHPFGTKVKVYITGHCQGTISW 324  
QY 207 NLACK-----PFWKPR-NLNISSQ-----SDMOVSPDHAFHGFREFYLYH 248  
DB 325 DMTCSFPIVLFLKQIDQDYSSRGNALTAHYDSNRLVSGDNGVLYRKPPEY 384  
QY 249 KLEH-----EGPEKR-----KTCQEQTTETTSCLLQWSP-----GDYIILY 287  
DB 385 LTEMSPFGSLKGNHIVQSVYIKLFGSLTCQKSNKHLAIGSDQGHSLVEVI 444  
QY 288 DDTNTRKVMHYALKPVSPWAGPIRIVTVPLVVISAFATLFT----- 332  
DB 445 D-----ALPTV-----LQVSLVDIEEAVNLVYTHIASDICPGIISLQ 482  
QY 333 -----VWCKKQENIYSHLDESSSTYTAALPRERLPRPFPKVFICYSSKO 380  
DB 483 PESCIYVQFEKNLVVYVAMRDSVFA-LDSDTGMIGNTKNPKP-----KPFKLYMQILD 536  
QY 381 GONEMNVVQCFAYFLQDPCGCEVALDWEFSLCRGQRENVQIKIESOPIIVVCS-- 437  
DB 537 GK-----QDTSG-----NGFDTSES-----TVEISIRQPSVLYCSEKA 571  
QY 438 -----KGMKTVKKNYKKG-----GGRSGKGLFVIVVASIAE-----K 474  
DB 572 YTYISLAHVQGVKVLHKKFESSPICASSTFYGTSGV---LTVFTDGTVEIRSLPE 628  
QY 475 LRQAKQS-----SSAALSKEFIATYDYSCEID-----VPGILDLSYRLMD 516  
DB 629 LSQLKQTSIRGPTSSPKNSLPETITASMDGLVWVMDGLVSVLPQKETFRLVE 688  
QY 517 NLPQLCSHLSRDLQEPQGHTRQGRSRR-----NYPSSKSGSLVAILCHNQPFIDE 570

Db 689 SM-----NRVYKDNVCHGIIITSSPREKSNPVSFKTKRITDTPESSSEYIEL 744  
 QY 571 POWKEQVPP-----HPPLRYREPVLKFD 598  
 Db 745 SKFTANFPNNVNSREINTITRVEDEELDIDDIDDDHHPNQQQKPKGIIIS 804  
 QY 599 GL-----VLNDVNCXKPGSPDFCLKVEAAVLAGTGPADGSDQSHSGGL 641  
 Db 805 GLSKQMARFESNFKGLKMAKNEKSVV-----TNDKEHEKNGATVDQIKKYGFTSS 860  
 QY 642 DQGEARALDGAALQPLLRHTVAGSPDMPRDSGLYDSSVSPSELSPLMLGSLTDTOT 701  
 Db 861 DENGAKNA-----QSKLOD-----NLAKIQISLRTT 888  
 QY 702 ETSSLTESVSSSS 714  
 Db 889 EMDYAKSESSTA 901

## RESULT 9

064634 ID 064634 PRELIMINARY; PRT: 2946 AA.  
 AC 064634  
 DT 01-AUG-1998 (Tremblrel. 07, Created)  
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE AL2945540 protein.  
 GN AT2945540  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.I., Mason T.M., Bowman C.B., Barnstead M.E., Feldblum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., VanAken S.E., Umayan L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,  
 RA Coppenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 thaliana."  
 RT thaliana.  
 RL Nature 402:761-768(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Lilo X.;

Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL; AC003680; AAC06163.1;  
 DR InterPro; IPR000409; Beige\_BEACH.  
 DR Pfam; PF02138; Beach; 1.  
 DR Pfam; PF00400; WD40; 3.  
 DR PRODOM; PD0000018; WD40; 1.  
 DR PRODOM; PD007848; Beige\_BEACH; 1.  
 DR SMART; SM00320; WD40; 3.  
 DR PROSITE; PS50197; BEACH; 1.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 KW Repeat; WD repeat.  
 SQ SEQUENCE 2946 AA; 321930 MW; B162CFBDEB5D3372 CRC64;

## Query Match

Best Local Similarity 2.94; Score 117; DB 10; Length 2946;

Matches 164; Conservative 105; Mismatches 314; Indels 294; Gaps 40;

QY 2 APLQLCSYFFTVNACLSQAVAGGSGRGARGADTCGWEMEAARPLCVANEGVGA 61

Db 393 ANWYIESPADTLNNAATAAAATAAAA-----ALSGKTSAMSAAMAS-----ALAGEG---- 441  
 QY 62 SRNSGLYNIFFKDNCTTILNPVGHVIAADQNTISQYACHQVAVTILMSFGALGIEF 121  
 Db 442 -----TAMPRLPFLSADNQGIEAFEA----- -QF 467  
 QY 122 LKGFVILEELKSGR-----QC-----OOLILKDPKOLNSFKRG 158  
 Db 468 L-----VYESSGKGRKSLHFTAFKPCQWYFGLHESCKQGLGKRAESLRLYIDGSL 522  
 QY 159 MESQPLAMKFTDYFVWVPPPSIKNESYHPFFF----- -TRACDLL 202  
 Db 523 YESREF-----DEPRISK-----PLSFCCIGTNPPTMAGLQRRCQPLF 563  
 QY 203 LO-----PDNLACKPFWKPNLNIHQGSDMVSFQHPHNFGRFFVLYHLKHKSGPPKRT 260  
 Db 564 AEMGPVYIFKEPIGPERMARLASRGDVLPCFNGA-----GLFWLATNYRN----- 612  
 QY 261 CQEQTTETTS-----CLLNVSFGDIIIELVDDTNTTK-----VMHYA-- 300  
 Db 613 -KAESSILDADIGGYTHLLYHPCLLSGRFPD--ASLSGAAGTLRRPAEVLQGVHVR 669  
 QY 301 LKPVHSPMA-----GPTRAVAITV-----PLDVISAFATLFTV----- 334  
 Db 670 MKPVESFWALAYGPASLLPLTVSVVHKDSLPCGLNPLSLSTVTLAAPPVFRIMVAIQ 729  
 QY 335 -----CRKQOE-----NIYSHLDEESSESTYTAALPRERLRPRKPVFLCTSSKDQGN 383  
 Db 730 HPGNEELCRTOGPETILARILSLVLSLHSLASLDKRDGVGEEL--VAALVSLCOSOR--IN 786  
 QY 384 HNVVQCAYFLQDFCGCEVALDWDNEDSLCREGQREWVIOKHESQFIIVVCSKGMK-- 441  
 Db 787 HVLYQLPFTLLD-----LKN-----SLCTGYLQKLLSLLDQMVTEATAMROAEAL 836  
 QY 442 -----YFVDKN-----YKHGGSGSGKGLFLVAVSAIAELKROAKOSSAA-- 485  
 Db 837 QLLDGGRCRCYWISEKNDSETTFPLDGNTRONGELNALDELIVIELLKGASPSLAND 896  
 QY 486 -LSKFIAYFYDSCGDPVGLDLSLTKYRLMDNI--POLCSHLESRDHGLQE-----PGQR 538  
 Db 897 DLRRLLGFIIDSPQNOVARVLHMLYRLVQPNARAOMFAEVFTTSGGIETLLVLQRE 956  
 QY 539 TROGRRNYFFSKSGSLYVAICNHQFIDEEDPWFKEQVFPFHPPLRYREPVLKFD 598  
 Db 957 AKTGEDNVLMGRSGKR-----SSTDPSKES--PYN-----ESGSVKQLDS 995  
 QY 599 GLVLNDV-MCKPGEPSDFCLKVEAAVLAGT--PADSOHESQMSGDDQDGEAKPALDGSAA 656  
 Db 996 NPEDNEIGFOLGPGDGN--SVEDDNVGSLVNPESVYRQKEHG----- -1035  
 QY 657 LQPLHETVAGSPDMPRDSGLYDSSVSPSELSPLMEGLSTDTOTETSLTESVSSSGL 716  
 Db 1036 -----STPVVCDUSVSISNINTERLS----- -AEIGGISLISADARS 1074  
 QY 717 GE-----EEPPA-----LPSKLLSGSGCKADLGCERS 742  
 Db 1075 MNVYNVDSAVVYVGIIRLIGALISSGHLTFDFDARS 1111

## RESULT 10

09KE04 ID 09KE04 PRELIMINARY; PRT: 901 AA.  
 AC 09KE04  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Transposase (08)/ABC transporter (ATP-binding protein).  
 GN BHI054.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=86665;  
 RN [1]



SEQUENCE FROM N.A.  
 RC STRAIN-C-125 / JCM 9153;  
 RA MEDLINE-20511584; PubMed-11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara M., Kubura S.,  
 RA Horikoshi K.L.,  
 RT Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis.\*;  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY  
 CC (ABC TRANSPORTERS).  
 DR EMBL: AF001510; BAB04773.1;  
 DR InterPro: IPR003593; AAA ATPase.  
 DR InterPro: IPR003439; ABC transporter.  
 DR InterPro: IPR002559; Transposase\_11.  
 DR Pfam: PF00005; ABC\_tran.1.  
 DR Pfam: PF01609; Transposase\_11.1.  
 DR ProDom: PD000006; ABC\_transporter.1.  
 DR SMART: SM00382; AAA.1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER.1.  
 KW ATP-binding; Transport; Complete proteome.  
 SQ SEQUENCE 901 AA; 104585 MW; E519406E650B2CBB CRC64;

Query Match 2.9%; Score 116.5; DB 16; Length 901;  
 Best Local Similarity 19.6%; Pred. No. 0.25;  
 Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;  
 QY 61 ASRNGSLNITFKYDNCITLNPVCKHVLAQNTISOT-ACHDOAVATILASPCALGI 119  
 DB 333 ALKESGL-----PLPTLIADAGYSGESNYVAMDELFELIPS----- 371  
 QY 120 EYLAGFVILEELKSGR-----CCOOL--ILEDKPOLNSFKRTGHESOPFLNKP 169  
 DB 372 ---HFR--QDARSFAKRPYINWRCDEDDVWCPNQRVSFKRTTRTOPY---GT 423  
 QY 170 ETDITV-----KVPP-PSI-----KNESHPFFTRACDILLQPDNLACKPMPKR 217  
 DB 424 ANDFKVIECEGCECPFECKTARGNQVHNPVY-----EELAKQHQKLK 471  
 QY 218 NLNISQHG-----SDMOVGFDAHPNFCFFFTYLYKLKHEGPKRTKCHQGTET 269  
 DB 472 ---SEGRITLYQRKTDVESVGHVQNLGFRLLRK----- 507  
 QY 270 TSCLLQVSPGDYIIELVDDVNTKRVNHALKPVESPWAGPIRAVAITVPLVVIS-APA 328  
 DB 508 ---ESVHIELGLVALAHNL 524  
 QY 329 TLTFTVCKKQENIYSHLDESSSTYTAALPRERLPKTVLCYSSKQCNHNVV 388  
 DB 525 KRATYDRSKPEPTNQHNRN-----RIKRP-----SRPYVL 558  
 QY 389 QCF---ATVLDGCGCEVALDWEFSLCGRQEW---IQKHESQFIIVVCSKGMK 441  
 DB 559 RCFWDSPPFKSDGKYASFALED---KLREGGENIEVIDLSKTYENROW---KGIN 612  
 QY 442 YFVDDKNTKHKGGSGSGGELFLVAVSAI-----AEKLRAKQSSSAALKS 488  
 DB 613 MEIERGEMVGLLPGNAGKSTTSMISLIQPTSGDVLKGSIHQSKAIRSILGVQ 672  
 QY 489 FIATYFDSCE-----GOVGLDLSKTYKLMNLPOLCSHLRSRHHGLQEPQITROG 542  
 DB 673 EIAYHDUTARENLAFTKIYGLKEELKHR-MESTLIQV-----GLEE-----RON 718  
 QY 543 SRNTRFSKGRSIIYAICNMHQ---FIDEEP 571  
 DB 719 DRVHTFGMKRRLNIAVALLHEPELIIMDEP 750  
 RESULT 11  
 ID 060669 PRELIMINARY; PRT; 938 AA.  
 AC 060669;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Protein kinase (Fragment).  
 GN EPHB3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95200798; PubMed-7893599;  
 RX Ruiz J.C., Conlon P.L., Robertson E.J.,  
 RT Identification of novel protein kinases expressed in the myocardium  
 RT of the developing mouse heart.\*;  
 RL Mech. Dev. 48:153-164(1994).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 DR EMBL: U11493; AAA67925.1;  
 DR EMBL: P29323; IB4F.  
 DR MGD: MGI:104770; Ephb3.  
 DR InterPro: IPR001030; Ephrin\_receptor.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003962; FNIII\_repeat.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR001660; SAM.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR InterPro: IPR001426; Kinase\_receptor.  
 DR Pfam: PF01404; EPHI\_lbd.1.  
 DR Pfam: PF00041; fn3.2.  
 DR Pfam: PF00069; pkinase.1.  
 DR Pfam: PF00536; SAM.1.  
 DR PRINTS: PR00014; FNTYPEIII.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase.1.  
 DR ProDom: PD001495; Ephrin\_receptor.1.  
 DR SMART: SM00060; FN3.2.  
 DR SMART: SM00454; SAM.1.  
 DR SMART: SM00119; TyrcK.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR.1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V.1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V.2.1.  
 KW Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat;  
 KW Transmembrane; Tyrosine-protein kinase.  
 FT NON\_TER 1  
 SQ SEQUENCE 938 AA; 103997 MW; 8D128CA46F19E73F CRC64;

Query Match 2.9%; Score 115.5; DB 11; Length 938;  
 Best Local Similarity 19.4%; Pred. No. 0.33;  
 Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;  
 QY 9 SVFTTVNACL-NGSOLAVA---AGGSGR---ARGADTCGWRMAAARPLC----- 52  
 DB 170 SLVIAPRACTIANAVFVSPLKLYCNGDEWHPVPGACTCATGHEPAKESQCRACPPGSY 229  
 QY 53 VANEVGVA-----SRNSG-----LYNTTFKYN-----CTTILNPGKHVTADQA 93  
 DB 230 KARQEGCPLCPNPNKRTTSPASICTCHNNFTRADSDSADACTRRSP-PRGVTSNV- 287  
 QY 94 NITISQACHDOAVATILMS-EGALGTEFLKGFVILEEK-SEG-----RQCQQLIL 144  
 DB 288 -----NETSLILENSEPRDLGGRRDOLLNVICKKRCGSGAGCATCRCDNVE 337  
 QY 145 KDPKOLNSFFRTGMESQPLNMFETDIYFKVVVPPPSIKNESNYHFFFTFRACDLIAQ 204  
 DB 338 FVPRQGLTERRVHS-----HLLAHTYTFEYQVNVGSGESPLPRYAAVNITNQAA 392  
 QY 205 PDNLACRFKFWKPNLNIISQSDMQVSEDFHAPNFGFRFFYLYKLKHEGFP-ARTCKQ 263

DB 393 PSEV-----PTLHSHSTSGSLTSLWAPPPNG---VLDYENKY---PEKSKAIA 439  
 QY 264 EOTTETSCILQNSP-GDYIIEVDVNTTKV-----MYALKPVHSPWAGPIRAVA 316  
 DB 440 TVTSQNSVLQLOPDAFVQV-----RAVTAGTQYTHPAEFITISERGSAQIQ 494  
 QY 317 ITVPLVISAFA-----TLTVWCKKQOENYSHLOESESSTYTAALPRELRP 368  
 DB 495 EQPLVIGSVAGVFWVVVVVIALVCLRKQH-----GDAETELK-QOYIAP 543  
 QY 369 RPKVFLYSSKQDNHNVQCFAYFLQDFC-GCEVALDLWEDFSLCRGOREWVIOKH 427  
 DB 544 GKMYIDPTTYEDPN--SAVREFAKIDVSCVKEEVIGAGEGEVCR-----589  
 QY 428 ESOFIIVCSKMGFYVDKYNHKGGRSGKGEFLVW/SAI-----AEKLRQAKOSS 483  
 DB 590 -----GRKLPGRRVEF-VAIKLVGVYTERQRDFLSEA 623  
 QY 484 AALSKFIATVFDYSCGDPGILDLS---TKYR-----LMDNLPOLCSHLRDRGLQ 333  
 DB 634 SNMGQF-----DHPNIRLBSVTVKSRPVMLTSEMENC-ALDGLRLND---667  
 QY 534 ERQOHT-----ROGSRNT-FESISGSLYV---AIC-----NMHQIDIE 569  
 DB 668 ---GGFTYIQLVGMIRGIAAGMKYLSMNTVHDLAARNILVNSLVCKYVDFGLSRFLD 725  
 QY 570 EPWFKEQF-----VFFH---PPPLRYREPVLKFDG-----GLVNDVMCKPGPE 612  
 DB 726 DPS--DPTTSSIGAKIDPWTAPEIAYR-----KFDASDVWSTGYVMVEVMS-----773  
 QY 613 SDFULVAAVLGATGPAQSOHESORGGLDQGEARPALDGSAAQLPLHTVYKAGSPSDM 672  
 DB 774 -----YGEOPYWMSNODDINAVEQDYRLPPMPCPTALHQLMASQWVRDNLRL 822  
 QY 673 PROSGIYD-----SSVPSSELSPLMEGLSTDTOT 701  
 DB 823 PKFSQIVNTLKLIRNAASLKVITASAPSG-MSQPLDRTVPDYT 865

## RESULT 12

Q99754 PRELIMINARY; PRT; 549 AA.  
 ID Q99754  
 AC Q99754; 1997 (Tremblrel. 03, Created)  
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC 2.7.1.68)  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97115834; PubMed=89551136;  
 RA Lofjens J.C., Anderson R.A.  
 RT "Type I phosphatidylinositol-4-phosphate 5-kinases are distinct  
 RT members of this novel lipid kinase family."  
 RL J. Biol. Chem. 271:32937-32943(1996).  
 DR ENBL; 078575; AAC50910.1;  
 DR InterPro; IPR002498; PIP5K.  
 DR Pfam; PF01504; PIP5K; 1.  
 DR SMART; SM00330; PIPK; 1.  
 KW Kinase; Transferase.  
 SQ SEQUENCE 549 AA; 61186 MW; 7CD48BFE17556A40 CRC64;

## Query Match

Best Local Similarity 18.18; Pred. No. 0.27;  
 Matches 121; Conservative 96; Mismatches 213; Indels 237; Gaps 32;

QY 114 PGALGTEFLK-GFRVILELKBGRCCQLILKDPKQLNSFRFTGNSOPFLMKKFTD 172  
 DB 41 PTASGMPFKIKGRVDSGGSTTKTKTSALKAIQIGITHTVGSLSKTPERDVLQDF 100

QY 173 YFVKVPPPS-----IKNESNVHPPFETTRACDLALLOFDNLACKPFWKPNLNISQBSOM 228  
 DB 101 YVESIFFPSSGSHWITPAHYNDPFEKYYA-----LHYLKHEGFPKKTCKQDPT 130  
 QY 229 QVSFDIAHPNGFR---FFY-----LHYLKHEGFPKKTCKQDPT 267  
 DB 131 PVAFRTRELGIIRPDYLYLSICSEPLIELCSGASGLFY-VSSDDEFFIKTVHKEAE 189  
 QY 268 ETTSCILQNSPQDYIIIEVDVNTTKVHYALKPVHSPWAGPIRAVAITVPLVISA 327  
 DB 190 -----FLQKLLPGTYM-----NLQNM-----PRTLLPKF 213  
 QY 328 ATLFTWCKKIQ-----OENYSHLOESESSTYTAALPRELRPRPRKVLCS 377  
 DB 214 YGLCYOAGGNIRIVVANNLLPRSVHMKIYDLKGSTYKRRASOKEREKPLP---T 267  
 QY 378 SKDQDNHNVQCFAYFLQDF-CGCEVALDLWEDFSLCRGOREWVIO---KHESOFII 433  
 DB 268 FKD-----LDLQDIPDGLFLDADNYN-ALCKTLQDCLVLSFKINDYSLLA 314  
 QY 434 VW-----CSKGMKYVDKNTKHKGGSGSGKGEFLVAVSAEKLRO-----477  
 DB 315 SINIDHOREPLSETQTSVDR-----RPAPKALYSTAMESQGFARRGGTNET 366  
 QY 478 -----AKOSSAALSKFIATVFDYSCGDPGILDSTKRYLMDNLPOLCSHL-HSR 528  
 DB 367 DBMGGIPARNSRGERLLLY-----GIIDILQSYRFPVKLEHSHKALYHDG 413  
 QY 529 DH-GLQEPQOHTQGRSRRTFRSKRSILYVAICNMQFTDEEPQWFKQVFPFPLR 587  
 DB 414 DTVSVHRCFGTAERFOR-----FMCN-----TVFKK--IPLKPSPK 448  
 QY 588 YREPVLEKFDGLVNDVMCKPGPESDFCLVAAVLGATGPAQSOHESORGGLDQGEA 647  
 DB 449 -----NFRSG---SFSRAGSGNSCITQPSVSG-----EHRAQ-----481  
 QY 648 RPALDGSALAPILHTVYKAGSPDMDPSGIYD-----SSVPSSELSPLMEGLSTDTOT 703  
 DB 482 ---VTKAEVPGVH---LGRPDVLFPQPLEEISEGSPIDPSFS-FLV-GETLQMLTY 533  
 QY 704 SSITESV 710  
 DB 534 STLEKL 540

## RESULT 13

Q9H460 PRELIMINARY; PRT; 348 AA.  
 ID Q9H460  
 AC Q9H460  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE BA425A6.2 (Similar to connexin) (Fragment)  
 CN BA425A6.2  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Heath P.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AL121749; CAC10186.1;  
 DR InterPro; IPR000500; Connexin.  
 DR Pfam; PF00029; connexin; 1.  
 DR PRINTS; PR00206; CONNEXIN  
 DR SMART; SM00037; CNX; 1.  
 DR PROSITE; PS00407; CONNEXINS\_1; 1.  
 DR PROSITE; PS00408; CONNEXINS\_2; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 348 AA; 37805 MW; 07EB6478067F8995 CRC64;



GenCore version 5.1.4.p5.4578  
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Old protein - protein search, using sw.model

Run on: May 19, 2003, 09:07:58 ; Search time 20.9109 Seconds  
(without alignments)  
1771.498 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_36\_313

Perfect score: 1515

Sequence: 1 ADTCGRKAAARPLCVAN.....RKVMYALKPVHSPWAGPIR 278

Scoring table: BLOSUM62

Gapop 10.0 , Gapert 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq.101002.\*

1:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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13:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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21:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	1515	100.0	753	23	ABB07626	Human cytokine rec
2	1509	99.6	753	23	ABB07627	Human cytokine rec
3	1427	94.2	554	23	AAU91330	Human novel secret
4	1427	94.2	739	23	ABB07628	Human cytokine rec
5	1423	93.9	738	22	AAU09904	Human Interleukin
6	1423	93.9	738	22	AAU09953	Human Interleukin
7	1423	93.9	738	22	AAU09954	Human Interleukin
8	1423	93.9	738	22	AAU09955	Human Interleukin
9	1423	93.9	738	22	AAU09956	Human Interleukin
10	1423	93.9	738	22	AAU09957	Human Interleukin

11	1416	93.5	738	22	AAU09951	Human Interleukin
12	1416	93.5	738	22	AAU09952	Human Interleukin
13	1389	91.7	738	22	AAU04938	Human Interleukin
14	1386	91.5	738	22	AAU04938	Human Interleukin
15	1343.5	88.7	738	22	AAU11355	Human DNAI cytokin
16	1334	88.1	296	22	AAU10601	5' portion of Huma
17	1290.5	85.2	739	23	ABB07630	Murine cytokine re
18	97	6.4	999	21	AAU33685	Arabidopsis thalia
19	97	6.4	1008	21	AAU33684	Arabidopsis thalia
20	97	6.4	1065	21	AAU33683	Arabidopsis thalia
21	92	6.1	1428	22	ABB5364	Arabidopsis thalia
22	89.5	5.9	368	19	AAU1360	Arabidopsis thalia
23	88	5.8	1173	23	ABB93479	Arabidopsis thalia
24	85.5	5.6	343	16	AAU73164	Arabidopsis thalia
25	85.5	5.6	654	22	AAU78776	Arabidopsis thalia
26	85	5.6	313	21	AAU79996	Arabidopsis thalia
27	85	5.6	340	21	AAU33643	Arabidopsis thalia
28	85	5.6	953	23	AAU51466	Arabidopsis thalia
29	85	5.6	980	23	AAU51467	Arabidopsis thalia
30	84.5	5.6	333	16	AAU73145	Arabidopsis thalia
31	84	5.5	333	21	AAU35508	Arabidopsis thalia
32	84	5.5	333	21	AAU35508	Arabidopsis thalia
33	83.5	5.5	343	16	AAU73147	Arabidopsis thalia
34	82.5	5.4	343	16	AAU73167	Arabidopsis thalia
35	82.5	5.4	343	16	AAU73150	Arabidopsis thalia
36	82.5	5.4	343	16	AAU73127	Arabidopsis thalia
37	82.5	5.4	520	23	ABB81643	Arabidopsis thalia
38	82.5	5.4	1276	22	ABB60848	Arabidopsis thalia
39	82	5.4	716	15	AAU55200	Arabidopsis thalia
40	82	5.4	716	20	AAU42473	Arabidopsis thalia
41	82	5.4	716	20	AAU81810	Arabidopsis thalia
42	82	5.4	716	21	AAU82208	Arabidopsis thalia
43	82	5.4	716	21	AAU82208	Arabidopsis thalia
44	82	5.4	716	21	AAU82208	Arabidopsis thalia
45	82	5.4	716	21	AAU82208	Arabidopsis thalia

## ALIGNMENTS

### RESULT 1

ABB07626

ID ABB07626 standard; Protein; 753 AA.

AC ABB07626;

DE 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 amino acid sequence.

DE Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human; pulmonary alveolar proteinosis; familial periodic fever; antitumor; erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

PN WC200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

PI (SYM) ZYNOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

PI WPI; 2002-217048/27.

PI N-PSDB; ABA95031, ABA95032.

PT New cytokine receptor polypeptide designated zcytor18, useful for inhibiting cell proliferation associated with psoriasis or tumor

growth, and modulating immune system by binding to endogenous zcytor18 ligand

Claim 1, Page 2; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 amino acid sequence.

Sequence 753 AA;

Query Match 100.0%; Score 1515; DB 23; Length 753;  
Best Local Similarity 100.0%; Pred. NO. 2.2e-161;  
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADTCGRKAAARPRLCVANEGVPSRNSGLYNTFKYDNTTYLNPVGRVIAQAQNI 60  
DB 36 ADTCGRKAAARPRLCVANEGVPSRNSGLYNTFKYDNTTYLNPVGRVIAQAQNI 95  
QY 61 TISQACHDQAVVITLSPGALGIEFLKGFVILELSEKSGRQCQQLIKDPQLNSSEK 120  
DB 96 TISQACHDQAVVITLSPGALGIEFLKGFVILELSEKSGRQCQQLIKDPQLNSSEK 155  
QY 121 RTGMESQPLNMFETDYFKVVPFSPKSNYHPPFTRACDILLQPDNLACPFWK 180  
DB 156 RTGMESQPLNMFETDYFKVVPFSPKSNYHPPFTRACDILLQPDNLACPFWK 215  
QY 181 PRLNISQSGDMQVSDHAPNFGFFFLYHLKHEGPFKTKCQBOQTTSCLIQ 240  
DB 216 PRLNISQSGDMQVSDHAPNFGFFFLYHLKHEGPFKTKCQBOQTTSCLIQ 275  
QY 241 NVSPGDYIIELVDVDTNTRKVMHYALKPVPSPWAGPIR 278  
DB 276 NVSPGDYIIELVDVDTNTRKVMHYALKPVPSPWAGPIR 313

RESULT 2

ID ABB07627 standard; Protein: 753 AA.

AC ABB07627;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, zcytor18 variant sequence.

KW Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;  
KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 269

FT /label= T269M

FT /note= "wild-type Thr is replaced with Met"

FT Misc-difference 750

FT /label= V750A

FT /note= "wild-type Val is replaced with Ala"

PN W0200208259-A2.

PD 31-JAN-2002;

PF 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

PA (ZYMO) ZYMOGENETICS INC.

PI Presnell SR; Kuestner RE, Gao Z;

DR WPI; 2002-217048/27.

DR N-PSDB; ABA95033, ABA95034.

PT New cytokine receptor polypeptide designated zcytor18, useful for  
PT inhibiting cell proliferation associated with psoriasis or tumor  
PT growth, and modulating immune system by binding to endogenous zcytor18  
PT ligand.

PS Disclosure; Page 94-98; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 variant amino acid sequence.

Sequence 753 AA;

Query Match 99.6%; Score 1509; DB 23; Length 753;

Best Local Similarity 99.6%; Pred. NO. 1.1e-160;  
Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADTCGRKAAARPRLCVANEGVPSRNSGLYNTFKYDNTTYLNPVGRVIAQAQNI 60  
DB 36 ADTCGRKAAARPRLCVANEGVPSRNSGLYNTFKYDNTTYLNPVGRVIAQAQNI 95  
QY 61 TISQACHDQAVVITLSPGALGIEFLKGFVILELSEKSGRQCQQLIKDPQLNSSEK 120  
DB 96 TISQACHDQAVVITLSPGALGIEFLKGFVILELSEKSGRQCQQLIKDPQLNSSEK 155  
QY 121 RTGMESQPLNMFETDYFKVVPFSPKSNYHPPFTRACDILLQPDNLACPFWK 180  
DB 156 RTGMESQPLNMFETDYFKVVPFSPKSNYHPPFTRACDILLQPDNLACPFWK 215  
QY 181 PRLNISQSGDMQVSDHAPNFGFFFLYHLKHEGPFKTKCQBOQTTSCLIQ 240  
DB 216 PRLNISQSGDMQVSDHAPNFGFFFLYHLKHEGPFKTKCQBOQTTSCLIQ 275  
QY 241 NVSPGDYIIELVDVDTNTRKVMHYALKPVPSPWAGPIR 278  
DB 276 NVSPGDYIIELVDVDTNTRKVMHYALKPVPSPWAGPIR 313

RESULT 3

ID AAU91330 standard; Protein: 554 AA.

AC AAU91330;

DT 18-JUN-2002 (first entry)

DE Human novel secreted protein LP253.

DE Human; secreted protein; cancer; autoimmune disease;

KW

arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease; meningitis; encephalitis; neoplasia; trauma; ischemia; infarction; stroke; myocardial infarction; atherosclerosis; sepsis; anemia; rheumatoid arthritis; hypothyroidism; allergic response; liver failure; multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder; autism; panic disorder; learning disability; feeding disorder; sleep pattern disorder; balance; perception; Th1-dependent insulinitis; adult respiratory distress syndrome; ARDS.

Homo sapiens.

WO200214358-A2.

21-FEB-2002.

30-JUL-2001; 2001WO-US211124.

11-AUG-2000; 2000US-224642P.

19-OCT-2000; 2000US-241779P.

(ELIL) LILLY & CO ELI.

Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;

WPI; 2002-304057/34.

N-PSDB; ABK62082.

Novel polypeptides and polynucleotides of secreted proteins useful for treating various diseases such as multiple sclerosis, cancer, autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's disease

Claim 9; Page 171-173; 235pp; English.

The invention relates to a novel human secreted polypeptide having a sequence 90% identical to the polypeptide sequences of LP105, LP061, LP224, LP239(a), LP243(a), LP243(b), LP253(b), LP218, LP251(a), LP252, LP239(b), LP255(a), LP255(b), LP244, LP186, LP251(b), LP255(b), LP223(b). Also included are the nucleic acids encoding the LP proteins (including complement, fragments encoding mature forms of the polypeptide or variant), a vector comprising the nucleic acid, a host cell comprising the vector, the preparation of the protein, an anti-LP antibody, ant/agonists of LP and anti-LP-encoding mRNA ribozymes. The secreted protein or its agonist is useful in the manufacture of a medicament for treating a mammal suffering from a disease (and in diagnosis), condition or disorder associated with aberrant levels of the secreted protein e.g. cancer, autoimmune diseases, arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease, meningitis, encephalitis, neoplasia, trauma, ischemia and infarction, stroke, cardiovascular disease, atherosclerosis, rheumatoid arthritis, hypothyroidism, anemia, sepsis, allergic responses, multiple sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive disorder, autism, panic disorder, learning disabilities, ALS (amyotrophic lateral sclerosis) psychoses, disorders in feeding, sleep patterns, balance, and perception. Th1-dependent insulinitis, adult respiratory distress syndrome (ARDS). The secreted protein is further useful for identifying compounds that bind to the secreted protein. The present sequence represents a novel secreted protein of the invention.

Sequence 554 AA;

Query Match 94.2%; Score 1427; DB 23; Length 554;  
Best Local Similarity 95.0%; Pred. No. 1.2e-151;  
Matches 264; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 AUTCGFRMAAARPLCVANEGVGPASRNSGLNITFKYDNCNTYLNVPVGRHYTADAQNI 60

DB 36 ADTCGR-----GGVPSRNSGLNITFKYDNCNTYLNVPVGRHYTADAQNI 81

QY 61 TISQYACHDQAVTILNSPGALGIEFLKGRVILEELKSGRCQOOLILKDPQLNSFK 120

DB 82 TISQYACHDQAVTILNSPGALGIEFLKGRVILEELKSGRCQOOLILKDPQLNSFK 141

QY 121 RTGNSQPLANKKETDYFVYVPPPSIKNSNTHPFFTRACDOLLLOPONLACRPFWR 180  
DB 142 RTGNSQPLANKKETDYFVYVPPPSIKNSNTHPFFTRACDOLLLOPONLACRPFWR 201  
QY 181 PRLNLSQSGDMQVSDHAPNFGFRFFLYLYLKHEGPFRRKTKCKOETTTSCLLQ 240  
DB 202 PRLNLSQSGDMQVSDHAPNFGFRFFLYLYLKHEGPFRRKTKCKOETTTSCLLQ 261  
QY 241 NVSPGDIYIELVDNTTRKVMHYALKPVHSPWAGPIR 278  
DB 262 NVSPGDIYIELVDNTTRKVMHYALKPVHSPWAGPIR 299

RESULT 4

ABB07628

ID ABB07628 standard; Protein; 739 AA.

XX AC ABB07628;

XX XX 20-MAY-2002 (first entry)

XX DE Human cytokine receptor, zcytor18 splice variant.

XX KW Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;  
XX KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
XX KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

XX OS Homo sapiens.

XX PN WO200208259-A2.

XX PD 31

XX PF 23-JUL-2001; 2001WO-US23253.

XX PR 26-JUL-2000; 2000US-220747P.

XX PA (ZIMO) ZYMOGENETICS INC.

XX PI Presnell SR, Kuestner RE, Gao J;

XX WPI; 2002-217048/27.

XX N-PSDB; ABA95035, ABA95036.

XX PT New cytokine receptor polypeptide designated zcytor18, useful for  
XX PT inhibiting cell proliferation associated with psoriasis or tumor  
XX PT growth, and modulating immune system by binding to endogenous zcytor18  
XX PT ligand

XX PS Claim 1; Page 102-106; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumor growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human zcytor18 splice variant.

Sequence 739 AA;

Query Match 94.2%; Score 1427; DB 23; Length 739;

Best Local Similarity 95.0%; Pred. No. 1.8e-151;

Matches 264; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 AUTCGFRMAAARPLCVANEGVGPASRNSGLNITFKYDNCNTYLNVPVGRHYTADAQNI 60

Db 36 ADTCGMR-----GVGPASRSLYNTFYDNCYTLNPKVGRVIADAQNI 81  
 QY 61 TISYACHDOVAVTILSPGALIEFLKGFVILELSEKRCQQLILKDPQLNSFK 120  
 Db 82 TISYACHDOVAVTILSPGALIEFLKGFVILELSEKRCQQLILKDPQLNSFK 141  
 QY 121 RTGESOFFLNMKFEDYFVKVPPSPKNSNYHFFFRACDILLQDNLACKPFWK 180  
 Db 142 RTGESOFFLNMKFEDYFVKVPPSPKNSNYHFFFRACDILLQDNLACKPFWK 201  
 QY 181 PRLNLSQHSQDMQVSFDHAPNFGFFFYLYHKLKHEGPKFKTKCKQBOETTTSCLLO 240  
 Db 202 PRLNLSQHSQDMQVSFDHAPNFGFFFYLYHKLKHEGPKFKTKCKQBOETTTSCLLO 261  
 QY 241 NVSPGDYIIELVDDTNTTKVNHVYALPVSHPWAGPIR 278  
 Db 263 NVSPGDYIIELVDDTNTTKVNHVYALPVSHPWAGPIR 299

## RESULT 5

AAU09904  
 ID AAU09904 standard; Protein: 738 AA.

AC AAU09904;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein.

Interleukin 17: hIL-17 receptor like protein; immunomodulatory;  
 anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 bone disease; vascular disorder; eye disorder; cancer; human.

OS Homo sapiens.

FN WO200168859-A2.

PD 20-SEP-2001.

PF 15-MAR-2001; 2001WO-US08678.

PR 16-MAR-2000; 2000US-189816P.

PR 28-NOV-2000; 2000US-0724460.

PA (AMGE-) AMGEN INC.

PI Jing S;

XX WPI; 2001-611392/70.

DR N-PSDB; AAS15346.

Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
 useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 diabetes, psoriasis and glaucoma

Claim 2; Page 152-154; 158pp; English.

The invention describes novel nucleic acids encoding Interleukin (IL) 17  
 receptor like polypeptides useful as vaccines and in gene therapy. These  
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 ophthalmological activities. The IL-17 receptor like nucleic acids and  
 proteins may be used to prevent and treat diseases associated with  
 inappropriate IL-17 receptor like polypeptide (hIL17r) expression. These  
 include, for example immune disorders (e.g. inflammation, diabetes and  
 transplant rejection), infections (e.g. hepatitis and septicemia),

CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17r may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17r antibodies and antagonists may also be used to down regulate  
 CC expression and activity. This is the amino acid sequence of the human  
 CC Interleukin 17 (IL-17) receptor like protein described in the method of  
 CC the invention.  
 XX  
 XX Sequence 738 AA;

Query Match 93.9%; Score 1423; DB 22; Length 738;

Best Local Similarity 94.9%; Pred. No. 5.2e-151;

Matches 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 2 DTGWRKAAARPLCVANECVGPASRSLYNTFYDNCYTLNPKVGRVIADAQNI 61

Db 37 DTGWR-----GVGPASRSLYNTFYDNCYTLNPKVGRVIADAQNI 82

QY 62 ISQYACHDOVAVTILSPGALIEFLKGFVILELSEKRCQQLILKDPQLNSFK 121

Db 83 ISQYACHDOVAVTILSPGALIEFLKGFVILELSEKRCQQLILKDPQLNSFK 142

QY 122 TGMESOFFLNMKFEDYFVKVPPSPKNSNYHFFFRACDILLQDNLACKPFWK 181

Db 143 TGMESOFFLNMKFEDYFVKVPPSPKNSNYHFFFRACDILLQDNLACKPFWK 202

QY 182 RLNLISQHSQDMQVSFDHAPNFGFFFYLYHKLKHEGPKFKTKCKQBOETTTSCLLO 241

Db 203 RLNLISQHSQDMQVSFDHAPNFGFFFYLYHKLKHEGPKFKTKCKQBOETTTSCLLO 262

QY 242 VSPGDYIIELVDDTNTTKVNHVYALPVSHPWAGPIR 278

Db 263 VSPGDYIIELVDDTNTTKVNHVYALPVSHPWAGPIR 299

## RESULT 6

AAU09953

ID AAU09953 standard; Protein: 738 AA.

AC AAU09953;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #3.

Interleukin 17: hIL-17 receptor like protein; immunomodulatory;  
 anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 363

XX /label- Ser, Thr, Ala, Cys

XX WO200168859-A2.



PD	20-SEP-2001.	DB	263	VSPGDYIIELVDVTNTTRKVMHVALKPVHSPWAGPIR	299
XX		RESULT 7			
PF	15-MAR-2001; 2001WO-US08678.	AAU09954			
XX		ID	AAU09954	standard; Protein; 738 AA.	
PR	16-MAR-2000; 2000US-189816P.	XX	AC	AAU09954;	
PR	28-NOV-2000; 2000US-0724460.	XX	DT	14-FEB-2002 (first entry)	
XX		XX	DE	Human Interleukin 17 (hIL-17) receptor like protein substitution #4.	
PA	(AMGE-) AMGEN INC.	XX	KW	Interleukin 17; hIL-17 receptor like protein; immunomodulatory.	
PI	Jing S;	XX	KW	anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;	
XX		XX	KW	hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;	
XX		XX	KW	anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;	
XX		XX	KW	vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;	
XX		XX	KW	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;	
XX		XX	KW	bone disease; vascular disorder; eye disorder; cancer; human; mutant;	
XX		XX	KW	muteln.	
XX		OS	OS	Homo sapiens.	
XX		OS	OS	Synthetic.	
XX		PH	Key	Location/Qualifiers	
XX		PH	Misc-difference 374	/Label- Val, Ile, Met, Leu, Phe, Ala, Nle	
XX		PT	WT	WO200168859-A2.	
XX		PT	20-SEP-2001.		
XX		PF	15-MAR-2001; 2001WO-US08678.		
XX		PR	16-MAR-2000; 2000US-189816P.		
XX		PR	28-NOV-2000; 2000US-0724460.		
XX		XX	(AMGE-) AMGEN INC.		
XX		PI	Jing S;		
XX		DR	WPI: 2001-611392/70.		
XX		PT	Nucleic acids encoding interleukin 17 receptor like polypeptides.		
XX		PT	useful for preventing, diagnosing and treating, e.g. leukemia, asthma,		
XX		PT	diabetes, psoriasis and glaucoma.		
XX		PS	Claim 21; Page -; 158pp; English.		
XX		CC	The invention describes novel nucleic acids encoding interleukin (IL) 17		
XX		CC	receptor like polypeptides useful as vaccines and in gene therapy. These		
XX		CC	have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,		
XX		CC	immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,		
XX		CC	anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,		
XX		CC	osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and		
XX		CC	ophthalmological activities. The IL-17 receptor like nucleic acids and		
XX		CC	proteins may be used to prevent and treat diseases associated with		
XX		CC	inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These		
XX		CC	include, for example immune disorders (e.g. inflammation, diabetes and		
XX		CC	transplant rejection), infections (e.g. hepatitis and septicemia),		
XX		CC	weight disorders (e.g. anorexia, cachexia and obesity), neuronal		
XX		CC	dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),		
XX		CC	lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease		
XX		CC	(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),		
XX		CC	bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders		
XX		CC	(e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and		
XX		CC	breast cancer), reproductive disorders (e.g. infertility and		
XX		CC	miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The		
XX		CC	DNA and its complements may also be used as diagnostic probes to detect and		
XX		CC	quantitate the presence of similar nucleic acids in samples and identify		
XX		CC	patients needing restorative therapy. The IL17rp may also be used as		
XX		CC	antigens in the production of antibodies against the proteins and in		
XX		CC	assays to identify modulators of expression and activity. The		
XX		CC	anti-IL17rp antibodies and antagonists may also be used to down regulate		
XX		CC	expression and activity.		
XX		CC	Note: This sequence is not given in the specification but is based on the		
XX		CC	human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)		
XX		CC	and has been created according to information given in claim 20.		
XX		XX	Sequence 738 AA;		
XX		XX	Query Match	93.98; Score 1423; DB 22; Length 738;	
XX		XX	Best Local Similarity	94.98; Pred. No. 5.2e-151;	
XX		XX	Matches 263; Conservative	0; Mismatches 0; Indels 14; Gaps 1;	
QY	2	DTGWRKMAARPRCLYANEGVGPASRNSGLYNITFKYDNTYLPVGVKRVIAQAQNT	61		
DB	37	DTGWR-----CVGPASRNSGLYNITFKYDNTYLPVGVKRVIAQAQNT	82		
QY	62	ISQYACHDQAVVTLWSPGALGIEFLKGFVILELKSSEKQCOQLIKDPQLNSSEK	121		
DB	83	ISQYACHDQAVVTLWSPGALGIEFLKGFVILELKSSEKQCOQLIKDPQLNSSEK	142		
QY	122	TGMSQPLNMEETDYKVVVPPSPKNSYNHFFPRTRACDQLLPDNLACKPFWKP	181		
DB	143	TGMSQPLNMEETDYKVVVPPSPKNSYNHFFPRTRACDQLLPDNLACKPFWKP	202		
QY	182	RNLISQSGDMQVDFDHPAHNFGFRFFLYLTKLKHGEPFRKTKQBOYTTTSCLIQ	241		
DB	203	RNLISQSGDMQVDFDHPAHNFGFRFFLYLTKLKHGEPFRKTKQBOYTTTSCLIQ	262		
QY	242	VSPGDYIIELVDVTNTTRKVMHVALKPVHSPWAGPIR	278		

CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rlp antibodies and antagonists may also be used to down-regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 21.  
 XX  
 SQ

Sequence 738 AA;

Query Match 93.9%; Score 1423; DB 22; Length 738;  
 Best Local Similarity 94.9%; Pred. No. 5.2e-151;  
 Matches 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 2 DTCGRWKAARPRCLVANGVGPAASRNSGLYNITFYDNCYTYLNPVGRVIADQAQNT 61  
 DB 37 DTCGRW-----GVPASRNSGLYNITFYDNCYTYLNPVGRVIADQAQNT 82  
 QY 62 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGROCOQLIKDPKOLNSFFKR 121  
 DB 83 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGROCOQLIKDPKOLNSFFKR 142  
 QY 122 TGMESQPLNKKFTDYFKVVPFSPKNSNHYHFKHKGPPKTKCKQBTETTSCLQN 181  
 DB 143 TGMESQPLNKKFTDYFKVVPFSPKNSNHYHFKHKGPPKTKCKQBTETTSCLQN 202  
 QY 182 RNLTISQSGDMQVSDHAPHNFGFRFFLYHLKHEGPPKTKCKQBTETTSCLQN 241  
 DB 203 RNLTISQSGDMQVSDHAPHNFGFRFFLYHLKHEGPPKTKCKQBTETTSCLQN 262  
 QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278  
 DB 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 299

# RESULT 8

AAU09955  
 ID AAU09955 standard; Protein: 738 AA.  
 XX  
 AC AAU09955;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.  
 XX  
 KW Interleukin 17; hIL-17 receptor like protein; Immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW muteln.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

FE Key Location/Qualifiers  
 FT Misc-difference 385  
 FT /label= Cys, Ser, Ala

XX WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX (AMGE-) ANGEN INC.

XX Jing S;

DR

XX

PT

PT

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PS

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WPI: 2001-611392/70

Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 diabetes, psoriasis and glaucoma

Claim 22; Page 7; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17  
 receptor-like polypeptides useful as vaccines and in gene therapy. These  
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 anti-parkinsonian, anti-convulsant, anti-leukaemic, dermatological,  
 osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and  
 ophthalmological activities. The IL-17 receptor like nucleic acids and  
 proteins may be used to prevent and treat diseases associated with  
 inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 include, for example immune disorders (e.g. inflammation, diabetes and  
 transplant rejection), infections (e.g. hepatitis and obesity), neuronal  
 weight disorders (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 dysfunction (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 breast cancer), reproductive disorders (e.g. infertility and  
 miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 DNA and its complements may also be used as diagnostic probes to detect and  
 quantify the presence of similar nucleic acids in samples and identify  
 patients needing restorative therapy. The IL17rlp may also be used as  
 antigens in the production of antibodies against the proteins and in  
 assays to identify modulators of expression and activity. The  
 anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 expression and activity.

Note: This sequence is not given in the specification but is based on the  
 human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 and has been created according to information given in claim 22.

Sequence 738 AA;

Query Match 93.9%; Score 1423; DB 22; Length 738;  
 Best Local Similarity 94.9%; Pred. No. 5.2e-151;  
 Matches 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 2 DTCGRWKAARPRCLVANGVGPAASRNSGLYNITFYDNCYTYLNPVGRVIADQAQNT 61  
 DB 37 DTCGRW-----GVPASRNSGLYNITFYDNCYTYLNPVGRVIADQAQNT 82  
 QY 62 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGROCOQLIKDPKOLNSFFKR 121  
 DB 83 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGROCOQLIKDPKOLNSFFKR 142  
 QY 122 TGMESQPLNKKFTDYFKVVPFSPKNSNHYHFKHKGPPKTKCKQBTETTSCLQN 181  
 DB 143 TGMESQPLNKKFTDYFKVVPFSPKNSNHYHFKHKGPPKTKCKQBTETTSCLQN 202  
 QY 182 RNLTISQSGDMQVSDHAPHNFGFRFFLYHLKHEGPPKTKCKQBTETTSCLQN 241  
 DB 203 RNLTISQSGDMQVSDHAPHNFGFRFFLYHLKHEGPPKTKCKQBTETTSCLQN 262  
 QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278  
 DB 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 299

## RESULT 9

AAU09956  
 ID AAU09956 standard; Protein: 738 AA.

XX AAU09956;

XX AC AAU09956;

XX 14-FEB-2002 (first entry)

XX

XX

XX

XX



CC immunosuppressive, hepatic, anabolic, anorectic, anti-asthmatic, dermatological,  
 CC anti-parkinsonian, anti-convulsant, anti-leukemic, anti-infectivity and  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rlp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 24.  
 CC  
 XX Sequence 738 AA;

Query Match 93.9%; Score 1423; DB 22; Length 738;  
 Best Local Similarity 94.9%; Pred. No. 5.2e-151;  
 Matches: 263; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 2 DTCGRKAAARPLCVANEGVPSRNSGLYNTFTYDNCYTLNPGVGHVADQNT 61  
 37 DTCGRK-----GVPSRNSGLYNTFTYDNCYTLNPGVGHVADQNT 82  
 62 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGRCQOLILKDPQLNSSFPR 121  
 83 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGRCQOLILKDPQLNSSFPR 142  
 122 TGESQPLANKFTDYFVKVYPPFSIKNSNTHPFFTRACDILLOPNLACKPFWKP 181  
 143 TGESQPLANKFTDYFVKVYPPFSIKNSNTHPFFTRACDILLOPNLACKPFWKP 202  
 182 RNLTISQSGSDQVSDPHAFNFGFRFFYLHKLKHEGPFKRTCKQDTTETTSCLQN 241  
 203 RNLTISQSGSDQVSDPHAFNFGFRFFYLHKLKHEGPFKRTCKQDTTETTSCLQN 262  
 242 VSPGDIYIELVDNTNTRKVMYALKPVHSPWAGPIR 278  
 263 VSPGDIYIELVDNTNTRKVMYALKPVHSPWAGPIR 299

## RESULT 11

ID AAU09951 standard; Protein; 738 AA.

AC AAU09951;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (IL-17) receptor like protein substitution #1.

KW Interleukin 17; IL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infectivity; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutuin.

OS Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 45 /label= Gly, Pro or Ala  
 PN WO200168859-A2  
 XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.  
 XX 16-MAR-2000; 2000US-189816P.  
 XX 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.

XX Jing S;

XX WPI; 2001-611392/70.

XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma -

XX Claim 18; Page -; 158pp; English.

XX The invention describes novel nucleic acids encoding Interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-leukemic, renal,  
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 XX include, for example immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infections (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of similar nucleic acids in samples and identify  
 XX patients needing restorative therapy. The IL17rlp may also be used as  
 XX antigens in the production of antibodies against the proteins and in  
 XX assays to identify modulators of expression and activity. The  
 XX anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 XX expression and activity.  
 XX Note: This sequence is not given in the specification but is based on the  
 XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 XX and has been created according to information given in claim 18.

XX Sequence 738 AA;

Query Match 93.5%; Score 1416; DB 22; Length 738;  
 Best Local Similarity 94.6%; Pred. No. 3.2e-150;

Matches 262; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

QY 2 DTCGRKAAARPLCVANEGVPSRNSGLYNTFTYDNCYTLNPGVGHVADQNT 61

DB 37 DTCGRK-----GVPSRNSGLYNTFTYDNCYTLNPGVGHVADQNT 82

QY 62 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGRCQOLILKDPQLNSSFPR 121

DB 83 ISQYACHDQVAVTILSPGALGIEFLKGFVILEELKSGRCQOLILKDPQLNSSFPR 142

QY 122 TGESQPLANKFTDYFVKVYPPFSIKNSNTHPFFTRACDILLOPNLACKPFWKP 181

Db 143 TGMESQPLNMFEDYFKVPPFSKNSYHFFRTACDLLODNLCKPFWKP 202  
 QY 182 RLNLISQSGSDMQVSDHAPNFGFRFFLYLKLKHEGPFRTCKQEQTTTSCLLQ 241  
 Db 203 RLNLISQSGSDMQVSDHAPNFGFRFFLYLKLKHEGPFRTCKQEQTTTSCLLQ 262  
 QY 242 VSPGDYIILVDYDNTTRVYHAYALKEVSPWAGPIR 278  
 Db 263 VSPGDYIILVDYDNTTRVYHAYALKEVSPWAGPIR-299

RESULT 12  
 AAU09952  
 ID AAU09952 standard; Protein: 738 AA.  
 AC AAU09952  
 XX  
 DT 14-FEB-2002 (first entry)  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #2.  
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmologic;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutin.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 227  
 FT /label= Phe, Leu, Val, Ile, Ala, Tyr  
 XX  
 PN WO200168859-A2.  
 PD 20-SEP-2001.  
 XX  
 XX 15-MAR-2001; 2001WO-US08678.  
 XX  
 PR 16-MAR-2000; 2000US-189816P.  
 PR 28-NOV-2000; 2000US-0724460.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 FI Jing S;  
 XX  
 DR WPI; 2001-611392/70.  
 XX  
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX  
 PS Claim 19; Page -: 158pp; English.  
 XX  
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmologic activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease

CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer); reproductive disorders (e.g. infertility and  
 CC miscarriage); eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rlp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 19.  
 SQ Sequence 738 AA:  
 Query Match 93.5%; Score 1416; DB 22; Length 738;  
 Best Local Similarity 94.6%; Pred. No. 3.2e-150;  
 Matches 262; Conservative 0; Mismatches 1; Indels 14; Gaps 1;  
 QY 2 DTCGWRMAAARPRLCVANEQVGPASRNSGLYNITFKYDNCITTLNPNVGVKHYADAQMIT 61  
 Db 37 DTCGWR-----GVGPASRNSGLYNITFKYDNCITTLNPNVGVKHYADAQMIT 82  
 QY 62 ISQYACHQDVAVTILMSPGALGIEFLKGFVILELSEKSGCQQLILKDPQLNSSEFKR 121  
 Db 83 ISQYACHQDVAVTILMSPGALGIEFLKGFVILELSEKSGCQQLILKDPQLNSSEFKR 142  
 QY 122 TGMESQPLNMFEDYFKVPPFSKNSYHFFRTACDLLODNLCKPFWKP 181  
 Db 143 TGMESQPLNMFEDYFKVPPFSKNSYHFFRTACDLLODNLCKPFWKP 202  
 QY 182 RLNLISQSGSDMQVSDHAPNFGFRFFLYLKLKHEGPFRTCKQEQTTTSCLLQ 241  
 Db 203 RLNLISQSGSDMQVSDHAPNFGFRFFLYLKLKHEGPFRTCKQEQTTTSCLLQ 262  
 QY 242 VSPGDYIILVDYDNTTRVYHAYALKEVSPWAGPIR 278  
 Db 263 VSPGDYIILVDYDNTTRVYHAYALKEVSPWAGPIR 299

RESULT 13  
 AAU04958  
 ID AAU04958 standard; Protein: 728 AA.  
 XX  
 AC AAU04958;  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE Human Interleukin 17 receptor, IL-17RH4.  
 XX  
 KW Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;  
 KW PRO20026; DNA 154095-2998; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 19..24  
 FT /note= "N-myristoylation site"  
 FT Modified-site 31..34  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 38..41  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 56..59  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 113..116  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 147..150



XX WPI; 2001-611392/70.  
DR N-PSDB; AAS16201.  
XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma.  
XX Claim 2; Fig 1; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and obesity), neuronal  
XX weight disorders (e.g. anorexia, cachexia and obesity), Parkinson's  
XX disease and epilepsy),  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantitate the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17rp may also be used as  
XX antigens in the production of antibodies against the proteins and in  
XX assays to identify modulators of expression and activity. The  
XX anti-IL17rp antibodies and antagonists may also be used to down regulate  
XX expression and activity. This is the amino acid sequence of human  
XX Interleukin 17 (IL-17) receptor like protein described in the method of  
XX the invention.  
XX Note: Residues 1-288 of this sequence correspond to residues 8-296 of the  
XX sequence shown in AAU10601 which is incomplete in the specification.

XX Sequence 739 AA;

Query Match 91.5%; Score 1386; DB 22; Length 739;  
Best Local Similarity 98.8%; Pred. No. 7.7e-147;  
Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 21 EVSGPASRNSGLYNTFYDNCITLYLNPVGRVIAQAQNIISQYACHQVAVTILSPG 80  
DB 42 QGVGPASRNSGLYNTFYDNCITLYLNPVGRVIAQAQNIISQYACHQVAVTILSPG 101  
QY 81 ALGIEFLKGRVILELSEKSGROCOQILKDPKQLNSFKETGMSQPLNKKFTDYFV 140  
DB 102 ALGIEFLKGRVILELSEKSGROCOQILKDPKQLNSFKETGMSQPLNKKFTDYFV 161  
QY 141 KVPFPSSIKNESYHFFRFRACDILLQPDNLACKPFWKPRNINISQSGSDQVSDHA 200  
DB 162 KVPFPSSIKNESYHFFRFRACDILLQPDNLACKPFWKPRNINISQSGSDQVSDHA 221  
QY 201 PHNGGFFPYLHYKLKHSQPKRCKQBQTTTSCLLQNVSPGYIIELVDDTNTTRK 260  
DB 222 PHNGGFFPYLHYKLKHSQPKRCKQBQTTTSCLLQNVSPGYIIELVDDTNTTRK 281  
QY 261 VMHYALKPVHSPWAGPIR 278  
DB 282 VMHYALKPVHSPWAGPIR 299

RESULT 15

ID AAU11355 standard; Protein: 738 AA.  
XX  
AC AAU11355;

XX 26-MAR-2002 (first entry)  
XX Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.  
DE  
XX Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;  
KW gene therapy; protein therapy; immunological disorder.  
KW  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 25 /label- Val  
FT /note- "Encoded by GTN"  
FT  
XX WO200190358-A2  
XX 29-NOV-2001.  
XX 23-MAY-2001; 2001WO-US16767.  
XX 24-MAY-2000; 2000US-206862P.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DW;  
XX WPI; 2002-106198/14.  
XX N-PSDB; AAS18134.  
XX Isolated antigenic human or mouse DNAX receptor subunit-like  
XX polypeptide useful for detecting antibodies generated in response to  
XX presence of increased protein levels or immunological disorders -  
XX  
XX Claim 1; Page 25; 148pp; English.

The invention relates to primate and rodent DNAX cytokine receptor  
XX subunit (DCRS) polypeptides and the polynucleotides encoding them. The  
XX receptors, or their portions may be useful as phosphate labelling enzymes  
XX to label general or specific substrates. The subunits may also be  
XX functional immunogens to elicit recognising antibodies, or antigens  
XX capable of binding antibodies. A combination, e.g., including a DCRS can  
XX be used as an immunogen for the production of antisera or antibodies  
XX capable of distinguishing between other cytokine receptor family members.  
XX A purified DCRS can also be used as a reagent to detect antibodies  
XX generated in response to the presence of elevated levels of expression,  
XX or immunological disorders which lead to antibody production to the  
XX endogenous receptor. This sequence represents the human DCRS8  
XX polypeptide.

XX Sequence 738 AA;

Query Match 88.7%; Score 1343.5; DB 23; Length 738;  
Best Local Similarity 90.6%; Pred. No. 4.8e-142;  
Matches 252; Conservative 2; Mismatches 9; Indels 15; Gaps 2;

QY 1 ADTCGRNRKAAARPLCVANEGVGPASRNSGLYNTFYDNCITLYLNPVGRVIAQAQNI 60  
DB 36 ADTCGRNRKAAARPLCVANEGVGPASRNSGLYNTFYDNCITLYLNPVGRVIAQAQNI 81  
QY 61 TISQYACHQVAVTILSPGALGIEFLKGRVILELSEKSGROCOQILKDPKQLNSSEK 120  
DB 82 TISQYACHQVAVTILSPGALGIEFLKGRVILELSEKSGROCOQILKDPKQLNSSEK 141  
QY 121 RTGMSQPLNKKFTDYFVKKVVPFSSIKNESYHFFRFRACDILLQPDNLACKPFWK 180  
DB 142 RTGMSQPLNKKFTDYFVKKVVPFSSIKNESYHFFRFRACDILLQPDNLACKPFWK 200  
QY 181 PRNLNISQSGSDQVSDHAFHNGFGRFFYLYKLKHSQPKRCKQBQTTTSCLLQ 240  
DB 201 PRNLNISQSGSDQVSDHAFHNGFGRFFYLYKLKHSQPKRCKQBQTTTSCLLQ 260  
QY 241 NVSPGYIIELVDDTNTTRKVMHYALKPVHSPWAGPIR 278



Mon May 19 09:52:38 2003

us-09-912-157-2\_copy\_36\_313.rag

Page 12

DB 261 NVSPGYIELVDDTTRKVNHYALKPVHSPHAGPIR 298

Search completed: May 19, 2003, 09:19:57  
Job time : 25.9109 sec

GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 10.263 seconds  
(without alignments)  
2604.041 million cell updates/sec

Title: US-09-912-157-2\_COPY\_36\_313  
Perfect score: 1515  
Sequence: 1 APTGCRKAAARPLCVAN.....RKVMHVALKPVHSPWAGPIR 278

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR73:

- 1: pir1.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	691	45.6	564	2 T42695	hypothetical prote
2	99	6.5	341	2 H71716	190 kd antigen pre
3	95	6.3	1462	1 B36182	protein-tyrosine-p
4	93	6.1	353	2 T33782	hypothetical prote
5	92	6.1	872	2 T25186	hypothetical prote
6	91.5	6.0	421	1 T28P1K	gene II protein -
7	91.5	6.0	758	2 T39210	3-isopropylmalate
8	88	5.8	1173	2 T51440	alpha-mannosidase
9	85.5	5.6	289	2 C36971	outer membrane pho
10	85.5	5.6	404	2 A28404	S-antigen - bovine
11	85	5.6	429	1 EHRT	Ig epsilon chain C
12	83	5.5	1121	2 T25715	hypothetical prote
13	82.5	5.4	420	2 T41870	ALK-EXO orf13 - B
14	82.5	5.4	461	2 T16225	hypothetical prote
15	82.5	5.4	622	2 T32757	hypothetical prote
16	82.5	5.4	1260	2 T20487	hypothetical prote
17	82	5.4	716	2 S70398	zona pellucida gly
18	81.5	5.4	320	1 A39479	hypothetical prote
19	81.5	5.4	839	2 F64171	hypothetical prote
20	81	5.3	286	2 D64400	hypothetical prote
21	80.5	5.3	363	2 S31780	peroxidase (EC 1.1
22	80.5	5.3	371	2 G85740	telcholic acid bios
23	80.5	5.3	498	2 H85040	hypothetical prote
24	80.5	5.3	526	2 T16124	hypothetical prote
25	80.5	5.3	538	2 T27433	hypothetical prote
26	80.5	5.3	670	2 AE2111	general secretion
27	80	5.3	2292	2 JCS561	capsid polyprotein
28	79.5	5.2	377	2 JCS569	heat shock protein
29	79	5.2	2102	2 T15626	hypothetical prote

30 78 5.1 571 2 T38759 probable pruvate  
31 78 5.1 612 2 E81287 probable sugar tra  
32 78 5.1 635 2 F81287 protein with DnaJ  
33 78 5.1 1014 2 H71602 190K antigen precu  
34 78 5.1 1795 2 F97713 phosphatase (acid  
35 78 5.1 2010 2 B71616 myosin X - bovine  
36 78 5.1 2052 2 T18519 myosin X - bovine  
37 77.5 5.1 226 2 AE1094 hypothetical prote  
38 77 5.1 512 2 C64599 hypothetical prote  
39 77 5.1 568 2 T39675 asparaginyl-trna s  
40 77 5.1 1420 2 S54471 probable membrane  
41 77 5.1 1589 1 RBYC5 cell division cont  
42 76.5 5.0 321 2 S78602 peroxidase (EC 1.1  
43 76.5 5.0 291 1 S28390 hemotetic protein m  
44 76.5 5.0 605 2 T07123 nine-cis-epoxycar  
45 76.5 5.0 711 2 T25281 hypothetical prote

## ALIGNMENTS

### RESULT 1

T42695

hypothetical protein DKFp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

C:Accession: T42695

R: Bloeker, H.; Boecker, M.; Brandt, P.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: 222230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFp434N1928

C:Genetics:

A:Note: DKFp434N1928.1

Query Match 45.6%; Score 691; DB 2; Length 564;

Best Local Similarity 99.2%; Pred. No. 2.9e-56;

Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 RPEFFFRACDILLQPNLACKPFRNLNLSQSGDMQVSDHAPNFCGPFYLYRK 214

DB 1 RPEFFFRACDILLQPNLACKPFRNLNLSQSGDMQVSDHAPNFCGPFYLYRK 60

QY 215 LKHEGPFKRTCKQPTTETSCLLQNVSPGDIYIELVDNTTRKVMHTALKPVHSPWA 274

DB 61 LKHEGPFKRTCKQPTTETSCLLQNVSPGDIYIELVDNTTRKVMHTALKPVHSPWA 120

QY 275 GP1R 278

DB 121 GP1R 124

RESULT 2

H71716

190 kd antigen precursor (scs2) RP081 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 03-Nov-2000

C:Accession: H71716

R: Andersson, S.G.E.; Zomrodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Almarik

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71716

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-341 <AND>

A:Cross-references: GB:AJ235270; GB:AJ235269; NID:93860572; PIDN:CAA14551.1; PID:9386

A:Experimental source: strain Madrid E

C:Genetics:

## A:Gene: sca2; RP081

Query Match 6.5%; Score 99; DB 2; Length 341;  
Best Local Similarity 22.1%; Pred. No. 0.21;  
Matches 69; Conservative 35; Mismatches 120; Indels 88; Gaps 15;

QY 15 RLGVANEVGPASR-----SGLNITP-----KYDNTIYLPVGVKVIADAO- 58  
DB 52 RLKVTIGAGDEKTVARGIWSGLGVNKGWKNPKIQGRIT-----GLTIGADAEF 106  
QY 59 -----NITISQACHDOVAVILMSPGALG-EFLGKRVILEEL 97  
DB 107 INNEHVGIVATSNLESIRKYNKLGKTAVEGHL-----SVYGLKELVKGFS--LQSI 157  
QY 98 KSGROCOOLILADPKOLNSP-KRTGMSQPLNKKFFYFVKKVPPFSIKNE-----S 152  
DB 158 TSTG---HNYIKNSKLNKIIGATQNNFOTLLNRYKYNLHFIPIGKYDYSRAS 214  
QY 153 NYHPFFETFRACDILLQPN-----LACKPFWPRN--LNISQSGSDMOVSPDH 199  
DB 215 NYKE--INVDIENLMIOKSNQSFSSIGAKIVSKPIISKNNILITLSAHG----- 263  
QY 200 APNFGFFETFLYKLGHEGPKRTCKQETTTSCLLQNVSPCDYIILEYDDNTNR 259  
DB 264 ---NIERNFNKNFVNAKFAKQTQETIIPKQPKLOYNI--GNMILASIKNINVL 318  
QY 260 KVHYALAPVHS 271  
DB 319 EYNIYTHKAYHS 330

## RESULT 3

B36182  
N:Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type PTP69D precursor - fruit fly  
A:Alternate names: protein-tyrosine-phosphatase DPTP  
C:Species: Drosophila melanogaster  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: B36182  
R:Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Salto, H.  
Proc. Natl. Acad. Sci. U.S.A. 86: 8698-8702, 1989  
A:Title: A family of receptor-linked protein-tyrosine phosphatases in humans and Drosophila  
A:Reference number: A36182; PMID:90046860; PMID:2534325  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1462 <STR>  
A:Cross-references: GB:M27699; MID:g158188; PIDN:AAA28842.1; PID:g158189  
C:Genetics:

A:Gene: Ptp69D  
A:Cross-references: FlyBase:FBgn0014007  
C:Superfamily: protein-tyrosine-phosphatase, receptor type PTP69D; fibronectin type III phosphatase homology  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-1462/Product: protein-tyrosine-phosphatase, receptor type PTP69D #status predicted  
F:29-806/Domain: extracellular #status predicted <EXT>  
F:38-114/Domain: immunoglobulin homology <IM1>  
F:147-316/Domain: immunoglobulin homology <IM2>  
F:807-823/Domain: transmembrane #status predicted <TMN>  
F:824-1462/Domain: intracellular #status predicted <INT>  
F:917-1145/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1213-1439/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:45-112,154-214/Disulfide bonds: #status predicted  
F:1097/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1103/Binding site: substrate phosphate (Arg) #status predicted  
F:1391/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1397/Binding site: substrate phosphate (Arg) #status predicted

## Query Match

Best Local Similarity 6.3%; Score 95; DB 1; Length 1462;  
Matches 67; Conservative 45; Mismatches 100; Indels 116; Gaps 18;

QY 20 NFGVGPASR-----NSGLNITFYID-----NCTYLNPVGVKHYADA 57

DB 259 NGNDPIOKFFIILQEGAGTPTTYHEDFINGSHSYLDEFPNTTYFLAYGKNSIGN 318  
QY 58 -----QNTISQACHDOV-----AVILMSPGALG-EFLGKRVILEEL 97  
DB 319 QPTQPGQITLST---DPFIKRVETGTASTITIGWNPDPDLIDYIOTIELIVSB- 374  
QY 98 KSGROCOOLILADPKOLNSP-KRTGMSQPLNKKFFYFVKKVPPFSIKNESYHPF 157  
DB 375 --SG-----EVPKIVIEALYQNSNLPYH-----FDKLTATDYE-- 408  
QY 158 FFRTRACDILLQPNLACKPFW-----KPRNLNISOH-----GSDMOVSF 197  
DB 409 -FRVACSDLTG---TCGP-NSENVGTMDGVATKPNLSIOCHDNVTRGNSIAINW 462  
QY 198 DHAPNFGFFETFLYKLGHE-----GPKRTCKQETTTSCLLQNVSPG-DY 247  
DB 463 DVPKTPNGKVVSYLILHGNPASTVDREMGPKIRIDEPHKT-----LYESVSPTNY 517  
QY 248 ILELYDDNTNR-----VMHYALKVHSP- 272  
DB 518 TVTYSATIRHKNGEPATGCLMPVSP- 345

## RESULT 4

T33782  
N:hypothetical protein C39F7.5 - Caenorhabditis elegans  
A:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T33782  
R:Maggi, L.; Scheet, P.; Dubbelde, C.  
submitted to the EMBL Data Library, October 1998  
A:Description: The sequence of C. elegans cosmid C39F7.  
A:Reference number: 221407  
A:Accession: T33782  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-353 <TAG>  
A:Cross-references: EMBL:AF101310; PIDN:AAC69214.1; GSPDB:GM000023; CESP:C39F7.5  
A:Experimental source: strain Bristol N2; clone C39F7  
C:Genetics:

A:Map position: 5  
A:Introns: 14/2; 45/3; 224/1  
C:Superfamily: Caenorhabditis elegans hypothetical protein C39F7.5

Query Match 6.1%; Score 93; DB 2; Length 3537  
Best Local Similarity 23.4%; Pred. No. 0.82;  
Matches 51; Conservative 24; Mismatches 65; Indels 78; Gaps 10;

QY 101 GRCQOOLILADPKOLNSP-KRTGMSQPLNKKFFYFVKKVPPFSIKNESYHPF 143  
DB 26 GLRSARNVLRATSGELAFSEFKRSSTRQIIRPFELIKSWPQDLNLLAEFAD--SKIL 83  
QY 144 PPSIKNESYHPFFTRACDILLQPNLACKPFWKPR---NLNI-----186  
DB 84 EF-----QRLCDNSKPTNSFLRDFESGTVSGNLTILFKFTSIRANRAF 128  
QY 187 -SQSGSDMOVS--FDHAPNHF-----GFRFFLYILKRGEPFKRTCKQEQ 230  
DB 129 VSORTNLKISANTYDENPENEDLCORLAFQDAVEIFLAKSYIYNQWENLGSMLQEQ 188  
QY 231 TTFETSCV-----LNQVSPGYIILEYDDNT 257  
DB 189 LCTDPCGFKKLEEDVETAKTKQDLKHGOLLIEVVDGKNT 226

## RESULT 5

T25186  
N:hypothetical protein T23F6.4 - Caenorhabditis elegans  
A:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T25186



Query Match 5.8%; Score 88; DB 2; Length 1173;  
 Best Local Similarity 21.8%; Pred. No. 12;  
 Matches 76; Conservative 38; Mismatches 102; Indels 132; Gaps 20;

QY 3 TCCHMKAAARPLCVANEGVGPASNSGLYNIFKYNCTTYTAPVKH-VIADAQNT 61  
 DB 346 TCG-----PEALCCOPD-----FARMG-----FYELC-----PQKHPTVETLENVQ 385  
 QY 62 ISQYACHOV-AYVILSPGALGIFLKGFRVI-LEELKSEGGCCQLILKPKQLNSF 119  
 DB 386 ERAKLLDOYRKSTLYRTNLLPLGGDFRYISIDSAQAFNTOMLF----- 434  
 QY 120 RTGMEOPFLN--MKFET--DYF-----YKVPFPPSKNE----- 151  
 DB 435 --DHINSNPLNAKAGTLEDFYFVREADRVNTRSPQVGVSGVYVGFSLSGDFFTY 492  
 QY 152 -----SNTH-----PEFFTRACDILQ-----PONLAC 175  
 DB 493 ADROQDYSGYVSRPF-----KAVDRVLEHTLGAETMSFLLGYCHRIDCEKFPSTFY 549  
 QY 176 KPEWKPRLNITSQSGDMQ-VSPDAPNFGFRFVLYLKLHKGPFKFTWC----- 226  
 DB 550 KLPAARNLALFQHDGVTGAKDYVDQYDTR---METSLOQLQIFMSAIEVLGIRH 506  
 QY 227 KQSTQTTISCLLVNSPGDYIELVDOTNTRKVMHYALKVPSFWA 274  
 DB 607 EKEKSO-----SPSFPEAQMS-----KYDARVPVKPIA 637

RESULT 9  
 C36971  
 outer membrane phospholipase A (EC 3.1.1.-) precursor - Proteus vulgaris  
 C:Species: Proteus vulgaris  
 C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 18-Jun-1999  
 C:Accession: C36971; S40130  
 R:Brok, R.G.P.M.; Brinkman, E.; van Bortel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tomm  
 J. Bacteriol. 176, 861-870, 1994  
 A:Title: Molecular characterization of enterobacterial pida genes encoding outer membran  
 A:Reference number: A36971; MUID:94131966; PMID:830539  
 A:Accession: C36971  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-289 <BR>  
 A:Cross-references: EMBL:X76902; NID:9436889; PIDN:CAA54224.1; PID:9436890  
 A:Note: authors translated the codon GAG for residue 74 as Gly and CGA for residue 115  
 C:Genetics:  
 A:Gene: pida  
 C:Superfamily: bacterial phospholipase A1  
 C:Keywords: carboxylic ester hydrolase

Query Match 5.6%; Score 85.5; DB 2; Length 289;  
 Best Local Similarity 26.5%; Pred. No. 3.1;  
 Matches 43; Conservative 16; Mismatches 59; Indels 45; Gaps 8;

QY 5 GWRMAARPLCVANEGV-----GPARNSGLYNITEKTN-----CTTYL 46  
 DB 6 GMLLAALPFPACAGNIDYKVDHPTAVRGSIIANNQEDHNPFTLYPESNYLLTYT 65  
 QY 47 NPVGRHVTAQNTISQYACHQVAVTI-----LMSGALGIEFLAGFRVILE---ELK 98  
 DB 66 SOLNKKAI---ESTYNSDNANKDEKFKLSLAPFLMR-GILGDSNLLGASTYQSRWOLLS 121  
 QY 99 SEGRCCOOLILKPKQLNSGFRKTCGSPFLANKPFTDFFV 140  
 DB 122 NTGE-----SAPRETNYEPQLFG--PATDYSV 148

RESULT 10  
 A28404  
 S-antigen - bovine  
 W:Alternate names: 48K rhodopsin-binding protein; arrestin  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 17-Nov-2000

C:Accession: B28404; A28404; A25826; A23619; S02144; S51073; I46054  
 R:Shiohara, T.; Dietzschold, B.; Craft, C.H.; Wistow, G.; Early, J.J.; Donoso, L.A.;  
 Proc. Natl. Acad. Sci. U.S.A. 84, 6975-6979, 1987  
 A:Title: Primary and secondary structure of bovine retinal S antigen (48-kDa protein)  
 A:Reference number: A28404; MUID:88041034; PMID:3478675  
 A:Accession: B28404  
 A:Molecule type: mRNA  
 A:Residues: 1-404 <SHI>  
 A:Cross-references: GB:J02955; NID:g162671; PIDN:AAA30378.1; PID:g162672  
 A:Accession: A28404  
 A:Molecule type: protein  
 A:Residues: 2-52; 56-66; 74-96; 103-117; 132-165; 176-236; 251-257; 299-308; 322-333; 355-367;  
 Biochem. Biophys. Res. Commun. 142, 904-910, 1987  
 R:Yamak, K.; Takahashi, Y.; Sakuregi, S.; Matsuura, K.  
 A:Title: Molecular cloning of the S-antigen cDNA from bovine retina.  
 A:Reference number: A25826; MUID:87156714; PMID:2950857  
 A:Accession: A25826  
 A:Molecule type: mRNA  
 A:Residues: 1-34; L' 36-118; V' 120-176; I' 178-316; B' 318-404 <VMS>  
 A:Cross-references: GB:M15115; NID:g162669; PIDN:AAA30377.1; PID:g162670  
 A:Experimental source: retina  
 A:Note: The authors translated the codon CTT for residue 35 as Val, GTG for residue 1  
 as Gln, and GAG for residue 379 as Gln  
 R:Wistow, G.J.; Kattal, A.; Craft, C.; Shiohara, T.  
 FEBS Lett. 196, 23-28, 1986  
 A:Title: Sequence analysis of bovine retinal S-antigen. Relationships with alpha-tran  
 A:Reference number: A23619; MUID:86108925; PMID:3080338  
 A:Accession: A23619  
 A:Molecule type: mRNA  
 A:Residues: 166-404 <WIS>  
 A:Cross-references: GB:X03454; NID:975; PIDN:CAA27179.1; PID:g76  
 R:Tsunasawa, S.; Shichi, H.  
 Biochim. Biophys. Acta 994, 191-193, 1989  
 A:Title: The amino acid sequence of S-antigen. N-terminus and uveitogenic peptides.  
 A:Reference number: S02144; MUID:89088273; PMID:2910351  
 A:Accession: S02144  
 A:Molecule type: Protein  
 A:Residues: 5-13; 198-229 <TS>  
 R:Kieselbach, T.; Irrgang, K.D.; Rueppel, H.  
 Eur. J. Biochem. 226, 87-97, 1994  
 A:Title: A segment corresponding to amino acids Val170-Arg182 of bovine arrestin is c  
 A:Reference number: S51073; MUID:95045604; PMID:7957262  
 A:Accession: S51073  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 170-182 <KIE>  
 R:Smith, W.C.; Millam, A.H.; Dugger, D.; Arendt, A.; Barygrave, P.A.; Palczewski, K.  
 J. Biol. Chem. 269, 15407-15410, 1994  
 A:Title: A splice variant of arrestin. Molecular cloning and localization in bovine r  
 A:Reference number: A54008; MUID:94253112; PMID:7515057  
 A:Accession: I46054  
 A:Molecule type: mRNA  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Residues: 1-369; A' <SMI>  
 A:Cross-references: EMBL:U08346; NID:g474378; PIDN:AAA20465.1; PID:g520467  
 C:Superfamily: arrestin  
 C:Keywords: blocked amino end; glycoprotein  
 F:1-404/Product: S-antigen, long form #status predicted <MAT>  
 F:5-404/Product: S-antigen, short form #status predicted <MAT>  
 F:170-182/Region: rhodopsin binding  
 F:1/Modified site: blocked amino end (Met) #status experimental  
 F:128-143/Diulfide bonds: #status predicted  
 F:228-271/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.6%; Score 85.5; DB 2; Length 404;  
 Best Local Similarity 20.6%; Pred. No. 4.9;  
 Matches 61; Conservative 32; Mismatches 88; Indels 115; Gaps 15;

QY 48 PVGKEV-----IADAQNTI-----SQYACH-----DQVAVTILMSFGALGIEFLAGFRVILE 95  
 DB 6 PAPHEVTFKAIKSRKSVTYLIGKRDYIDHVERVEPVGWLVDP-----ELVKGKRVTV- 59  
 QY 96 ELKSEGGCCOOLILKPKQLNSGFRKTCGSPFLANKPFTD-YFVWVVPFSI----- 148

RESULT 12  
T257115  
Hypothetical protein F19F10.11a - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T257115  
R:Kellen, J.; Wamsley, P.  
A:Submitted to the EMBL Data Library, April 1997  
A:Description: The sequence of *C. elegans* cosmid F19F10.  
A:Reference number: Z20073  
A:Accession: T257115  
A:Status: preliminary; translated from GB/EMBL/DDbJ  
A:Molecule type: DNA  
A:Residues: 1-1121 <REL>

A; Experimental source: strain Bristol N2; clone FL19F10  
C: Genetics:

A.Gene:	CESP.F19F10.11a
A.Map position:	5
A.A.Ions:	19/3; 54/2; 87/2; 120/2; 162/2; 187/2; 337/2; 432/2; 466/3; 833/2; 889/2
Query Match	5.5%; Score 83; DB 2; Length 1121;
Best local Similarity	24.3%; Pred. No. 32;
Matches	50; Conservative 79; Mismatches 79; Indels 48; Gaps 10;
QY	79 PGALGIEFLGRFVILEELKSGRCQQQLIKDPKQNSFKRTGMESQPF--LNMFFT 136
DB	769 PRLAEEIETPAI-----PEIRSSQQIAGPSETLDKDVKQEITTEEFKITYKREA 822
QY	137 -----DYEV-KVPFPFSINKSNT--HPFFER-TRACD---LLLPDLNACKPFWMAPRL 184
DB	823 VBEDEYEVEIREIPADSPAEITLERPKAFWFKTSKYDAIKAAAKDKPKAPKVVPVST 882
QY	185 NTSIQSGDMOVSFDHAPHNFGRFYLIYKLKHGEPRFKRTQEQBTETTSCLLGNVSP 244
DB	883 SCVOGTG-----EHGLRRKRSDPDOR----LPFLNNAVRK 915

245	GOYIELVDNTNTTRKVVHYALKPVH	270
	: :	
	: :	
916	GAIPLETPPI-FRRKAIFFCLEKH	940

RESULT 13

741870

ALK-EXO orf133 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C:Species: Bombyx mori nuclear polyhedrosis virus, *BuSNPV*

A:Variety: isolate T3

C:\Date:\03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:\Accession: T41870  
R:\Com1, S.; Majima, K.; Maeda, S.  
J. Gen. Virol. 80, 1323-1337, 1999

A, Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.  
A, Reference number: Z2020; MUID: 99781911; PMID: 10355780  
A, Accession: T41870  
A, Status: preliminary; translated from GB/EMBL/DDBJ

A: Molecule type: DNA  
A: Residues: 1-420 <KAM>  
A: Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63799.1; PID:g3745952  
A: Experimental source: isolate T3

C: Genetics;  
A: Note: alk-exo  
C: Superfamily: OpMPV alkaline exonuclease

Query Match 5.43; Score 82.5; DB 2; Length 420;  
Best Local Similarity 21.28; Pred. No. 9.8;  
Matches 48; Conservative .27; Mismatches 74; Indels 77; Gaps 11;

[illegible]

90 KOBGKQCUILLADPQUINSEFAK-----TUMESLIFE LUNATE ELDI- FIVVFFPSLN 149

|::| |::||| :| |::| |:





GenCore version 5.1.4.p5.4578  
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OK protein - protein search, using sw model

Run on: May 19, 2003, 09:08:53 Search time 5.64467 Seconds  
(without alignments)  
2042.709 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_36\_313

Perfect score: 1515

Sequence: 1.ADTGWRKAAARPLCVAN.....RKVMYALAPVSPWAGPIR 278

Scoring table: BLOSUM62

Gapop 10.0, Gapert 0.5

Searched: 112892 seqs, 4147328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	95	6.3	1462	1	PTP6_DROME
2	91.5	6.0	421	1	VG2_BPIKE
3	91.5	6.0	758	1	LEU2_SCHPO
4	85.5	5.6	289	1	PAL_PROVU
5	85.5	5.6	404	1	ARRS_BOVIN
6	85	5.6	429	1	EPC_RAT
7	84	5.5	405	1	ARRS_PIG
8	84	5.5	449	1	MCEI_CANAL
9	82	5.4	716	1	EP2_FELCA
10	81.5	5.4	320	1	MEC3_CAEVU
11	81.5	5.4	839	1	KDRA_HAELN
12	81	5.3	286	1	Y804_METUA
13	80.5	5.3	363	1	PER_COPCI
14	80.5	5.3	364	1	PER_ARTRA
15	79	5.2	405	1	ARRS_CANFA
16	78	5.1	518	1	TBX5_HUMAN
17	78	5.1	571	1	DCPI1_SCHPO
18	78	5.1	2052	1	MY10_BOVIN
19	77.5	5.1	1001	1	TP3A_HUMAN
20	77	5.1	1420	1	Y48B_YEAST
21	77	5.1	1589	1	CC25_YEAST
22	76.5	5.0	321	1	MEC3_CAREL
23	76.5	5.0	770	1	LEU2_CANMA
24	76.5	5.0	3433	1	UTRO_HUMAN
25	76	5.0	295	1	MEC3_CAEBR
26	76	5.0	342	1	LYCA_BPCP7
27	76	5.0	456	1	Y172_DROME
28	76	5.0	518	1	TBX5_MOUSE
29	76	5.0	537	1	SYR_MYCPN
30	76	5.0	566	1	X397_MYCGE
31	76	5.0	858	1	STVL_VIBCH
32	76	5.0	2290	1	POLG_EMCV
33	75.5	5.0	667	1	VTER_HSV6U

#### RESULT 1

ID	PTP6_DROME	STANDARD	PRT	1462 AA
AC	P16620			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase).			
GN	PTP69D OR DPTP			
OS	Drosophila melanogaster (Fruit fly)			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila			
OC	NCBI_TaxID=7227			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=90046860; PubMed=2554325;			
RX	Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.,			
RT	"A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).			
CC	- FUNCTION: IT IS POSSIBLE THAT DPTP IS A CELL ADHESION RECEPTOR.			
CC	- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H2O -> protein tyrosine + phosphate.			
CC	- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL; M27699; AAA28842.1;			
DR	PIR; B36182; B36182			
DR	HSSP; P18052; IYPO			
DR	FlyBase; FBgn0014007; Ptp69D			
DR	InterPro; IPR003961; FN.III			
DR	InterPro; IPR003006; IG_MHC			
DR	InterPro; IPR003598; IG_C2			
DR	InterPro; IPR003600; IG_Like			
DR	InterPro; IPR00387; TYR_phosphatase			
DR	Pfam; PF00041; fn3; 3			
DR	Pfam; PF00047; Ig; 2			
DR	Pfam; PF00102; Y_phosphatase; 2			
DR	PRINTS; PR00700; PTPPHPTASE			
DR	SMART; SM00060; FN3; 3			
DR	SMART; SM00410; IG_Like; 1			
DR	SMART; SM00408; IGC2; 1			
DR	SMART; SM00194; PTPC; 2			

074770 schizosacch  
P57528 buchera ap  
P24731 autographa  
P37609 lactococcus  
Q91684 xenopus lae  
P37078 klebsiella  
O44220 drosophila  
P27558 human papil  
P05129 homo sapien  
Q98r17 homo sapien  
P17181 homo sapien  
O29753 archaeoglob

#### ALIGNMENTS

DR PROSITE; P500383; TYR PHOSPHATASE 1; 2.  
 DR PROSITE; P500556; TYR PHOSPHATASE 2; 2.  
 DR PROSITE; P500557; TYR PHOSPHATASE 2; 2.  
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 KW Cell adhesion; Immunoglobulin domain; Repeat.  
 FT SIGNAL 1 23  
 FT CHAIN 24 1462 PROTEIN-TYROSINE PHOSPHATASE DPTP  
 FT DOMAIN 24 805 EXTRACELLULAR (POTENTIAL)  
 FT TRANSMEM 806 823 POTENTIAL  
 FT DOMAIN 824 1462 CYTOPLASMIC (POTENTIAL)  
 FT DOMAIN 147 221 IG-LIKE C2-TYPE DOMAIN 1  
 FT DOMAIN 332 437 FIBRONECTIN TYPE-III 1  
 FT DOMAIN 438 538 FIBRONECTIN TYPE-III 2  
 FT DOMAIN 912 1165 PROTEIN-TYROSINE PHOSPHATASE 1  
 FT DOMAIN 1208 1459 PROTEIN-TYROSINE PHOSPHATASE 2  
 FT ACT\_SITE 1097 1097 BY SIMILARITY  
 FT ACT\_SITE 1391 1391 BY SIMILARITY  
 FT DISULFID 45 112 POTENTIAL  
 FT DISULFID 154 214 POTENTIAL  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 58 58 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 64 64 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 162 162 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 196 196 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 209 209 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 288 288 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 429 429 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 451 451 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 516 516 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 613 613 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 701 701 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 755 755 N-LINKED (GLCNAC) (POTENTIAL)  
 SQ SEQUENCE 1462 AA; 167411 MW; F8091D69888230EB CRC64;  
 Query Match 6.38; Score 95; DB 1; Length 1462;  
 Best Local Similarity 20.4%; Pred. No. 1;  
 Matches 67; Conservative 45; Mismatches 100; Indels 116; Gaps 18;  
 QY 20 NEGVPASR-----NSGLNITPKYD-----NCTTILNPGVGRHVIADA 37  
 DB 259 NQDNDIQRFITLQEAQTFTHEDFNGSHSTSYLDHFKNPTTYELRVGKNSIGNG 318  
 QY 58 -----QNITISQACHDQV-----AVTILMSPGALG-IEFLAGFRVILEEL 97  
 DB 319 QPTQYPOGITTLSY---DPFIKPVETGVTASTITIGNPPPDLDIYIYELVSE- 374  
 QY 98 KSEKQCQQLIKDPKOLNSSFRTGMSQPPFLANKETDYFKVVPVPSIKNESYHP 157  
 DB 375 --SG-----EYKVEIAIYQNSRLPYM-----FDKLKATDYE-- 408  
 QY 158 FFRTRACDLILQPNLACKPFW-----KPRMLNISOR-----GSDMQVSP 197  
 DB 409 -FVRACSDLRK---TCGP-WSENVNGTMDGVATPTNLSICQHDNVTIRGNSIAINW 462  
 QY 198 DHAPHNFGFRFYLYLKHKE-----GPFKRTCKEQTTFETTSCLIQVSPQ-DY 247  
 DB 463 DVEKTPNGKVVSYLIHLGNPASTVDREMGWPKIRRIDEPHKI-----LYESVSPNTN 517  
 QY 248 IIELVDDVTNTRK---VNHVALKPVHSP 272  
 DB 518 TVTVSAITRHKNGEPATGSLMPYSTP 545

RESULT 2

VG2\_BPIKE STANDARD; PRT; 421 AA.  
 AC P03560;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Gene II protein [Contains: Gene X protein].  
 GN II AND X.  
 OS Bacteriophage Ite.  
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.  
 OX NCBI\_TaxID=10867;  
 RN RP-SEQUENCE FROM N.A.  
 RX MEDLINE=85160831; PubMed=3981635;  
 RA Peeters B.P.H., Peters R.M., Schoenmakers J.G.G., Konings R.N.H.,  
 RT "Nucleotide sequence and genetic organization of the genome of the N-  
 specific filamentous bacteriophage Ite. Comparison with the genome of  
 the P-specific filamentous phages M13, fd and f1".  
 RT J. Mol. Biol. 181:27-39(1985)  
 RL J. Mol. Biol. 181:27-39(1985)  
 CC -I- FUNCTION: GENE II PROTEIN IS REQUIRED FOR DNA REPLICATION. THE  
 CC FUNCTION OF THE GENE X PROTEIN IS UNKNOWN.  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@sib-sib.ch).  
 CC EMBL; X02139; CAA26067.1;  
 DR EMBL; X02139; CAA26068.1;  
 DR PIR; A04265; Z2BPIK.  
 KW DNA replication; Alternative initiation.  
 FT CHAIN 1 421 GENE II PROTEIN.  
 FT CHAIN 301 421 GENE X PROTEIN.  
 FT INIT\_MET 301 301 FOR GENE X PROTEIN  
 SQ SEQUENCE 421 AA; 47594 MW; 626AC1FDDFAE5215 CRC64;  
 Query Match 6.08; Score 91.5; DB 1; Length 421;  
 Best Local Similarity 21.4%; Pred. No. 0.47; Mismatches 44; Indels 119; Gaps 18;  
 Matches 71; Conservative 44;  
 QY 10 AARPRLCVANEVGVGPARNSGLYNITFKYDNCNTTILNPGVGRHVIADAQNTISQVACHD 69  
 DB 123 AAMPPEL-----YDLCDVTNTVGR-----IDVTSKAVAND 154  
 QY 70 QVA-----VTILNSPGALGIEFLAGFRVILEELKSEGRQCC 105  
 DB 155 HIANOVISFLRNSNGQTKTRALDYETTVANEGS-----RHTLVATLKHHEVQAO 207  
 QY 106 QLILADPKOLN-SSFKRTGME--SOPFLNMFETDYFKVVPVPSIKNESYHPFFRT- 161  
 DB 208 IRELKQKSSHLTYIENCLVLSNPDLQL-----YAVGLVRF-----EALHTRFFENF 257  
 QY 162 -----RACDLILQPD-----NLAKPFWK--RNLNISQSGSDMV-----SFDHAPHN 203  
 DB 258 GLPRFFFDIVTYQNYEGSSFNLC-DLWKKSKFDLDFAKGSDMNVYDDSKVDALINN 316  
 QY 204 FGF-----RFFLYHLKHEGPFKRTCKEQBT-----ETTS-----CLL 239  
 DB 317 FSVVTRKSGNISNSKANLFGFYRLVNEG-YDNVAQTMERTTFRSLKELTVGLSKAOL 375  
 QY 240 QNVSPCDYIIELVDDTNT--TRKVMHYALKPV 269  
 DB 376 MNLSTNNVNVLPVQMINVDVFSQQYPTWVPEV 407  
 RESULT 3  
 LEU2\_SCHPO STANDARD; PRT; 758 AA.  
 AC O14289;  
 DT 15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)  
13-JUN-2002 (Rel. 41, Last annotation update)  
3-isopropylmaleate dehydratase (EC 4.2.1.33) (Isopropylmaleate isomerase) (Alpha-IPM isomerase) (IPMI)  
SPAC39.03  
Schizosaccharomyces pombe (Fission yeast)  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes  
NCBI\_Taxid:4896;  
[1]  
SEQUENCE FROM N.A.  
SPR1AW-972;  
MEDLINE:21848401; PubMed:11859360;  
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sournay J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth I., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moute S., Mungall K., Murphy L., Niblett D., Odeall C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkart G., Aert R., Robben J., Grynoprez B., Weltyens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert R., Beyer P., Zimmermann W., Nedler H., Wambutt R., Purnelle B., Pohl T.M., Goffeau A., Cadieu E., Dreano S., Gloux S., Melaine V., Mottier S., Galibert F., Naves S., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G., Daya R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L., Cerrutti L., Lowe T., McComb M.W., Paulsen I., Potashkin J., Sipakowski G.V., Ussery D., Barrell B.G., Nurse P.;  
"The genome sequence of Schizosaccharomyces pombe";  
Nature 415:871-880(2002)  
-1- FUNCTION: Catalyzes the isomerization between 2-isopropylmaleate and 3-isopropylmaleate, via the formation of 2-isopropylmaleate.  
-1- CATALYTIC ACTIVITY: 3-isopropylmaleate -> 2-isopropylmaleate + H(2)O.  
-1- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O -> 2-isopropylmaleate.  
-1- PATHWAY: Leucine biosynthesis; second step.  
-1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.  
-----  
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-----  
EMBL: Z99262; CAB16402.1;  
InterPro: IPR000573; Aconitase\_C.  
InterPro: IPR001030; Aconitase\_N.  
InterPro: IPR004430; Leuc.  
InterPro: IPR004431; Leud.  
Pfam: PF00330; aconitase; 1.  
PRINTS: PR00415; ACONITASE.  
ProDom: PD000511; Aconitase\_N; 1.  
TIGRFAMs: TIGR00170; leuc; 1.  
TIGRFAMs: TIGR00171; leud; 1.  
PROSITE: PS00450; ACONITASE\_1; 1.  
PROSITE: PS01244; ACONITASE\_2; 1.  
Leucine biosynthesis; lyase; Iron-sulfur; 4Fe-4S.  
METAL 359 359 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
METAL 420 420 IRON-SULFUR (4FE-4S)

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FT METAL: 423 423 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 758 AA; 82782 MW; CE78C3682838847 CRC64;

Query Match 6.0%; Score 91.5; DB 1; Length 758;
Best Local Similarity 24.6%; Pred No: 0.98;
Matches: 51; Conservative 22; Mismatches: 85; Indels 49; Gaps 10;

QY 10 AARPRLCVANEVGVPASNSGLNYTFKYDCTVILNPGVKV-----TADAQNTTIS 63
DB 466 AAIKGHLCNVEEPGGVDSNGSPSIITNKPDSHDVSGDIGLSVODATDVTADGLANN 525
QY 64 QYACHEDVAVYILNSGALGIEFLKGRFVILELSESGRCOCQILILEPKOLNSSPKFG 123
DB 526 -----VAGSV--SGSGAGIPKTVETGIALPAPMANVTDKII--PQGLTKIRKG 573
QY 124 MESQFLKAKFEYDIFKVVVPPSKKNESNYHFFFRACDILLQPNLACKPFWKPRN 183
DB 574 LGQAFYFIRYDAD--GKEIP-DVFLAREY-----RHATVIVAHNFGC----- 615
QY 184 LNTSQSGDMQVSDRAP-----HNFGFR 207
DB 616 -----GS-----SREHAPWALNDFGIR 632

RESULT 4
PAL_PROVU STANDARD; PRT; 289 AA.
AC PAL_PROVU
ID P37447;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Phospholipase A1 precursor (EC 3.1.1.32) (Detergent-resistant
DE Phospholipase A) (DR-phospholipase A) (Phosphatidylcholine 1-
DE phospholipase) (Outer membrane phospholipase A) (OM PLA)
DE PLDA.
GN Proteus vulgaris.
OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OS Proteus.
OC NCBI_TAXID=585;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=94131966; PubMed=8300539;
RX Brok R.G.P.M., Brinkman E., van Bortel R., Bekkers A.C.A.P.,
RA Verheij H.M., Tommassen J.;
RT "Molecular characterization of enterobacterial plda genes encoding
RT outer membrane phospholipase A."
RL J. Bacteriol. 176:861-870(1994).
CC -1- FUNCTION: HYDROLYSIS OF PHOSPHATIDYLCHOLINE WITH PHOSPHOLIPASE
CC A2 (EC 3.1.1.4) AND PHOSPHOLIPASE A1 (EC 3.1.1.32) ACTIVITIES.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O - 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O - 2-
CC acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: REQUIRES CALCIUM IONS FOR ACTIVITY.
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE; ONE OF THE VERY FEW ENZYMES
CC LOCATED THERE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X76302; CAAS4224.1; -3-
CC DR PIR: C36971; C36971.
CC DR PIR: S40130; S40130.
CC DR HESP: P00631; IQD6.
CC DR InterPro: IPR003187; PfAM.
CC DR Pfam: PF02253; PfAM; 1.
CC DR PRINTS: PR01486; PHEPLIPASEA1.
CC DR Hydrolase: Lipid degradation. Outer membrane; Signal; Calcium
CC KW

```

FT SIGNAL 1 20 BY SIMILARITY  
 FT CHAIN 21 289 PHOSPHOLIPASE A1  
 FT ACT\_SITE 164 164 BY SIMILARITY  
 SQ SEQUENCE 289 AA: 3294 MW: D75516OFFB406997 CRC64;  
 Query Match 5.69; Score 85.5; DB 1; Length 289;  
 Best local similarity 26.59; Pred. No. 1.1;  
 Matches 43; Conservative 16; Mismatches 58; Indels 45; Gaps 8;  
 QY 5 GWRMAARPRUCVANEV-----GPSRNSGLYNITFKYN-----CTYL 46  
 DB 6 GMLAAALPFAACQAEATIDKVDTPAVRGSIAMQEDNEPFLYPIESNYLLTYT 65  
 QY 47 NPVGHVIAQAQNTISOTACHQDVAVTI-----LWSPGALGIEFLKGRVILE---ELK 98  
 DB 66 SDLNKKAI-----ESYNWSNANKDEVKFQLSIAFLWR-GILGNSILGASYTORSMWOLS 121  
 QY 99 SEGRCCOOLIKDPKQLNSFKRGMESQFLNMFETDIFV 140  
 DB 122 NTGB-----SAPFRENTYERQLELG--FATDYSV 148  
 RESULT 5  
 ARRS\_BOVIN STANDARD; PRT; 404 AA.  
 AC P08166;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE S-arrestin (Retinal S-antigen) (48 kDa protein) (S-AG) (Rod  
 DE photoreceptor arrestin).  
 GS SAG.  
 GN Bos taurus (Bovine).  
 OC Eukaryota; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88041034; PubMed=3478675;  
 RA Shinohara T., Dietzschold B., Craft C.M., Wistow G., Early J.J.,  
 RA Donoso L.A., Horwitz J., Tao R.;  
 RT "Primary and secondary structure of bovine retinal S antigen (48-kDa  
 RT protein).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6975-6979(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=87156714; PubMed=2950857;  
 RA Yamaki K., Takahashi Y., Sakuregi S., Matsubara K.;  
 RT "Molecular cloning of the S-antigen cDNA from bovine retina.";  
 RL Biochem. Biophys. Res. Commun. 142:904-910(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE=94253112; PubMed=7515057;  
 RA Smith W.C., Millam A.E., Dugger D., Arendt A., Hargrave P.A.,  
 RA Palczewski K.;  
 RT "A splice variant of arrestin. Molecular cloning and localization in  
 RT bovine retina.";  
 RL J. Biol. Chem. 269:15407-15410(1994).  
 RN [4]  
 RP SEQUENCE OF 166-404 FROM N.A.  
 RX MEDLINE=86108925; PubMed=3080338;  
 RA Wistow G.J., Katial A., Craft C.M., Shinohara T.;  
 RT "Sequence analysis of bovine retinal S-antigen. Relationships with  
 RT alpha-transducin and G-proteins.";  
 RL FEBS Lett. 196:23-28(1986).  
 RN [5]  
 RP SEQUENCE OF 1-12 AND 198-229.  
 RX MEDLINE=89088273; PubMed=2910351;  
 RA Tsunashima S., Shichi H.;  
 RT "The amino acid sequence of S-antigen: N-terminus and uveitogenic  
 RT peptides.";

RL Blochim. Biophys. Acta 994:191-193(1989).  
 RN [6]  
 RP CALCIUM-BINDING DATA  
 RX MEDLINE=90264449; PubMed=2160981;  
 RA Huppertz B., Weyand I., Bauer P.J.;  
 RT "Ca<sup>2+</sup>-binding capacity of cytoplasmic proteins from rod  
 RT photoreceptors is mainly due to arrestin.";  
 RL J. Biol. Chem. 265:9470-9473(1990).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).  
 RX MEDLINE=98154736; PubMed=9495348;  
 RA Granzin J., Wilden U., Choe H.W., Labahn J., Krafft B., Buldt G.;  
 RT "X-ray crystal structure of arrestin from bovine rod outer segments.";  
 RL Nature 391:918-921(1998).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=99235986; PubMed=10219246;  
 RA Hirsch J.A., Schubert C., Gurevich V.V., Sigler P.B.;  
 RT "The 2.8 Å crystal structure of visual arrestin: a model for  
 RT arrestin's regulation.";  
 RL Cell 97:257-269(1999).  
 CC -1- FUNCTION: ARRESTIN IS ONE OF THE MAJOR PROTEINS OF THE ROS  
 CC (RETINAL ROD OUTER SEGMENTS); IT BINDS TO PHOTONCTIVATED-  
 CC PHOSPHORYLATED RHODOPSIN, THEREBY APPARENTLY PREVENTING THE  
 CC TRANSDUCED-MEDIATED ACTIVATION OF PHOSPHODIESTERASE.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM (P44); ARE PRODUCED BY ALTERNATIVE SPLICING. THE SHORT  
 CC FORM PLAYS A ROLE IN THE PHOTOTRANSDUCTION CASCADE.  
 CC -1- TISSUE SPECIFICITY: RETINA AND PINEAL GLAND. THE P44 ISOFORM IS  
 CC LOCALIZED IN THE PHOTORECEPTOR OUTER SEGMENT.  
 CC -1- DISEASE: S-ANTIGEN INDUCES AUTOIMMUNE UVEITIS.  
 CC -1- MISCELLANEOUS: ARRESTIN BINDS CALCIUM.  
 CC -1- SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.  
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 DR EMBL; J02955; AAA30378.1;  
 DR EMBL; M5115; AAA30377.1;  
 DR EMBL; U08346; AAA20465.1;  
 DR EMBL; X03454; CAA27179.1;  
 DR PIR; A23619; A23619.  
 DR PIR; A28404; A28404.  
 DR PIR; S02144; S02144.  
 DR PIR; A25826; A25826.  
 DR PDB; 1AYR; 13-JAN-99.  
 DR PDB; 1CFI; 16-APR-99.  
 DR InterPro; IPR000698; Arrestin.  
 DR Pfam; PF00339; arrestin; 1.  
 DR Pfam; PF02752; arrestin\_C; 1.  
 DR PRINTS; PR00309; ARRESTIN.  
 DR PRODOM; PD002099; Arrestin; 1.  
 DR PROSITE; PS00295; ARRESTINS; 1.  
 DR Sensory transduction; Vision; Autoimmune uveitis; Acetylation;  
 DR Sensory transduction; Vision; Acetylation (IN 30% OF THE CHAINS).  
 KW Calcium-binding; Alternative splicing; ACETYLATION (IN 30% OF THE CHAINS).  
 FT MOD\_RES 1 1  
 FT PROPEP 1 4  
 FT DISULFID 128 143  
 FT VARSPLIC 370 370  
 FT VARSPLIC 371 404  
 FT CONFLICT 35 35  
 FT CONFLICT 119 119  
 FT CONFLICT 177 177  
 FT CONFLICT 317 317  
 FT SEQUENCE 404 AA; 45275 MW; 26B1D80B652AF1EF CRC64;  
 SQ  
 Query Match 5.69; Score 85.5; DB 1; Length 404;  
 Best Local Similarity 20.69; Pred. No. 1.6;

Matches 61; Conservative 32; Mismatches 88; Indels 115; Gaps 15;

OY 48 PVCKEV---TADAONTI---SOYACK---DOVAVTILSPGALGIEFLAFVILELSEGGCOOLILKDP 112  
 DB 6 PARNVIFKISRKQVYILKRDYIDHVERPEVGVLDVP-----ELVGRKVVY- 59  
 OY 96 ELKSGROCOOLILKDPKLNSTFRTGSGQPLNKKFTD-IPVKKVPPPSI-----148  
 DB 60 -----SLTCAF-RYQGEDIDVGLSPFRDLTFSQVQVFPVPGASGAT 100  
 OY 149 -----KNESYHFFFRACDILLOPDMLACKPFWKPRNLNISO-----188  
 DB 101 TLOSLIKLKANTYF-----LLTPDYLPQVLMQAPQDVGKSGVDFEIKAF 152  
 OY 189 -HGSDMOV-----SFDHAPNFG-----S-PRFYLHYLK-----216  
 DB 153 ATHTSDVEEDIPKSSVLLIKYQVHAPRDMGQPPRAASQPFASDKPLRLAVLSKE 212  
 OY 217 -----HGSPK---RTCKQRTTETSCLLQNS-----PGDIILVDDNTTRKY 261  
 DB 213 IYHGEPIPVTVNSTKTKIKVLVEQVTVNVLSSDIYIKTVAEEAQEKY 268

# RESULT 6

ID EPC\_RAT STANDARD; PRT: 429 AA.

AC P01855;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig epsilon chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 [1]  
 SEQUENCE FROM N.A. (IMMUNOCTOMA IR2).  
 RC STRAIN=LOU/C/NSL;  
 RX MEDLINE=83064537; PubMed=6992865;  
 RA Helman L., Petterson U., Engstrom A., Karlsson T., Bennich H.;  
 RT "Structure and evolution of the heavy chain from rat immunoglobulin E";  
 RL Nucleic Acids Res. 10:6041-6049(1982).  
 [2]  
 SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).  
 RX MEDLINE=83182019; PubMed=6020340;  
 RA Kindavogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;  
 RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, identification, and DNA sequence";  
 RL DNA 1:335-343(1982).  
 [3]  
 SEQUENCE OF 205-306 FROM N.A.  
 RX MEDLINE=82174576; PubMed=6803238;  
 RA Helman L., Petterson U., Bennich H.;  
 RT "Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).

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CC EMBL; J00744; AAA41379.1; ALT\_INIT.

DR PIR; A02143; EHRT.  
 DR HSP; P01854; LIGE.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig\_4.

DR SHANT; SM00410; IG-like; 3.  
 DR SHANT; SM00407; IGL1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT CONFLICT 168 168 R->N (IN REF. 2).  
 FT CONFLICT 308 308 P->L (IN REF. 2).  
 SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;

Query Match 5.6%; Score 85; DB 1; Length 429;

Best Local Similarity 18.6%; Pred. No. 2;

Matches 52; Conservative 42; Mismatches 92; Indels 94; Gaps 11;

OY 56 DRONTITISOTAC---HDVAVTILSPGALGIEFLAFVILELSEGGCOOLILKDP 112  
 DB 115 NAFSTIOLICFYGHIONDSIEN-----LMDRKIYETHAGNVLKEE 159  
 OY 113 KQLNSTFRTGSGQPLNKKFTDIPVKKVPPPSIKNESNTHPFFTRACD-----165  
 DB 160 GKLASTYSRLNITQQQWMS---ESTFTCKVT-----SOGENTWATRCSDDEPRGV 208  
 OY 166 --LLQPDNLACKPFWKPR-----NLNIS-----OHGSDMOVSDHAPHN- 203  
 DB 209 IYLLPPSPDLIYNGTPKLCTCLVLDLSEENITVTVWRERKKSIGSASQSTKH--HNA 266  
 OY 204 -----FGFRFYLHY-----KLKEGPKFKTC-----KOE 229  
 DB 267 TTSITSLPVDKMDIEGSGYQCRVDHPHPKPIVSITKAPGRSAPEVTVLPPEEE 326  
 OY 230 QTETTSCLLQNSPGDIILVDDNTTRKYMKYALKPV 269  
 DB 327 KDKRTLCLIONFFPDISVQWLQDSKLIPKSORSTTTP 366

# RESULT 7

ID ARRS\_PIG STANDARD; PRT: 405 AA.

AC P79260;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE S-arrestin (Retinal S-antigen) (48 kDa protein) (S-AG) (Rod  
 DE photoreceptor arrestin).  
 GN SAG.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxID=3623;  
 [1]  
 SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=96273620; PubMed=8690040;  
 RA Singh A.K., Kumar G., Shinohara T., Shichi H.;  
 RT "Porcine S-antigen: cDNA sequence and expression in retina, ciliary  
 RT epithelium and iris";  
 RL Exp. Eye Res. 62:299-308(1996).  
 CC 1- FUNCTION: ARRESTIN IS ONE OF THE MAJOR PROTEINS OF THE ROS  
 CC (RETINAL ROD OUTER SEGMENTS); IT BINDS TO PHOTOACTIVATED-  
 CC PHOSPHORYLATED RHODOPSIN, THEREBY APPARENTLY PREVENTING THE  
 CC TRANSDUCIN-MEDIATED ACTIVATION OF PHOSPHODIESTERASE.  
 CC 1- TISSUE SPECIFICITY: RETINA AND PINEAL GLAND. ALSO EXPRESSED IN THE  
 CC ANTERIOR TISSUES SUCH AS THE CILIARY EPITHELIUM AND IRIS  
 CC EPITHELIUM.  
 CC 1- DISEASE: S-ANTIGEN INDUCES AUTOIMMUNE UVEITIS.  
 CC 1- SIMILARITY: ARRESTIN BINDS CALCIUM (BY SIMILARITY).  
 CC 1- SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.

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CC DB EMBL: S82664; AAB46757.2; 1CPI  
 DR HSSP: P08168; 1CPI  
 DR InterPro: IPR000698; Arreclin.  
 DR Pfam: PF00339; arreclin.1  
 DR Pfam: PF02732; arreclin.C.1  
 DR PRINTS: PR00309; ARRESTIN  
 DR PROSITE: PS002099; ARRESTIN.1  
 DR PROSITE: PS002295; ARRESTINS.1  
 DR Sensory transduction; vision; Autolimmune uveitis; Calcium-binding  
 FT DISULFID 131 146  
 SQ SEQUENCE 405 AA; 45102 MW; F9C0C8658C8FA73E CRC64;

Query Match 5.5%; Score 84; DB 1; Length 405;  
 Best Local Similarity 21.5%; Pred. No. 2.3;  
 Matches 68; Conservative 31; Mismatches 97; Indels 120; Gaps 17;

QY 19 ANEGVGPASRNSGLNITFKYDNCCTYINPVGKRVIAQAQNTISQYACH-DQAVV---T 74  
 DB 3 ANVQASKSTENHVFYFKTSRDKSVTYL---GKR-----DYIDVDQVEPVGV 48  
 QY 75 ILASPGALGIEFLKGFVILIELSEGRQCOQILKDPKQLNSFKTNGESQPLNKF 134  
 DB 49 VLVDP-----ELVGRKRVV-----SUTCAP-RYQGDIDVIGLSF 83  
 QY 135 EFD-IFVYVVPPFSI-----KNESNYHPPFFTRACOLLQPDNLACKPFW 179  
 DB 84 RDLIFSVQVQVPPVGAASQTKLQESLIKKLGHTYFP-----LTFPDLFPCSYML 135  
 QY 180 KPRNLISQ-HGSDMQV-----SFOHAPNPF-----SFOHAPNPF----- 205  
 DB 136 QPAPQDVKGCGVDPEKAFATSDADGDKIPKSSVRLIRKRVQVHAPLENGPQPHAEA 195  
 QY 206 -PREFY-----LHVKLK-----HEGPFK---RKCKOEOTTTSCLLQVYS 245  
 DB 196 AQOFNSDKELHITVSLSKELYTHGEIPVTVTNTEKTKIKALVEQVANNVLYSS 255  
 QY 246 DYIELVDNTTRKY 261  
 DB 256 DYIKPVATEEQKV 271

RESULT 8  
 ACCEL\_CANAL STANDARD; PRT; 449 AA.  
 ID P78587;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE mRNA capping enzyme alpha subunit (mRNA guanylyltransferase)  
 DE (EC 2.7.7.50) (GTP--RNA guanylyltransferase) (Gtase).  
 GN CGRI.  
 OS Candida albicans (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5476;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-IFO 1060;  
 RX MEDLINE=96425877; PubMed=8828219;  
 RA Yamada-Okabe T., Shimm O., Doi R., Mizumoto K., Arisawa M.,  
 RA Yamada-Okabe H.;  
 RT "Isolation of the mRNA-capping enzyme and ferric-reductase-related  
 RT genes from Candida albicans";  
 RL Microbiology 142:2515-2523(1996).  
 CC -1- FUNCTION: SECOND STEP OF mRNA CAPPING. TRANSFER OF THE GMP MOIETY  
 CC OF GTP TO THE 5' END OF RNA YIELDING A 52 KDa ENZYME-GMP COVALENT  
 CC REACTION INTERMEDIATE.  
 CC -1- CATALYTIC ACTIVITY: GTP + (5')ppp-mRNA - diphosphate +  
 CC G(5')ppp-mRNA.  
 CC -1- SUBUNIT: THE mRNA CAPPING ENZYME IS COMPOSED OF TWO SEPARATE  
 CC CHAINS ALPHA AND BETA, RESPECTIVELY A mRNA GUANYLYLTRANSFERASE AND

AN RNA 5'-TRIPHOSPHATASE.  
 -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC GTASE FAMILY.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 CC  
 DR EMBL: D83180; BAAL1833.1;  
 DR InterPro: IPR001339; mRNA\_cap\_enzyme.  
 DR Pfam: PF01331; mRNA\_cap\_enzyme.1.  
 KW Transferase; Nucleotidyltransferase; mRNA processing; mRNA capping;  
 KW Nuclear protein.  
 FT ACT\_SITE 67 67 GUANYLYLATION SITE (POTENTIAL).  
 FT DOMAIN 427 435 POLY-GLN  
 SQ SEQUENCE 449 AA; 52253 MW; D93P448F11305BB CRC64;

Query Match 5.5%; Score 84; DB 1; Length 449;  
 Best Local Similarity 20.4%; Pred. No. 2.6;  
 Matches 56; Conservative 34; Mismatches 92; Indels 92; Gaps 13;

QY 79 PGALGIEFLKGFVILIELSEGRQCOQILKDPKQLNSFKTNGESQPLNKF 139  
 DB 41 PGSPQVSFER--RLEETLMAQDIFVCENTDGLRCLFLINDPD-----KGEV---F 88  
 QY 130 LNKRFETDFVAVVPPFSIKNESNYHPPFFTRACD-LIOPDNLACKPFWK 180  
 DB 89 LVTRENDYIFIPNIHFPLSVNETREKPTVHGTLLDGLVELNENVS-EPVLRTVIFDAL 147  
 QY 181 -----PRNL-----NISQSDMQVSDFAHNPFGFFVLYR--- 213  
 DB 148 AIHGKCIIDRLPKLGLYITENVAKPDPNFKHNPDI-VNSPEFPKVGFKTLTSTHAD 206  
 QY 214 -----KLHGEPKRTKCKQEQTTTSCLLQVSPG-----DIILV----- 252  
 DB 207 DVLSEMDKLFLHASDGLIYCAETPYVFGDTQLKRWPAENTVDQLEFVENEVQDPDL 266  
 QY 253 DDTNTTKVMHYALAP-----VHSPWA 274  
 DB 267 DERDPTSTLYDPAKPNLIKLRVWQGSNVHTDFA 300

RESULT 9  
 ID ZP2\_FELCA STANDARD; PRT; 716 AA.  
 AC P47984;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE zona pellucida sperm-binding protein 2 precursor (zona pellucida  
 DE glycoprotein ZP2) (zona pellucida protein A).  
 GN ZP2 OR ZPA.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=95143578; PubMed=7841460;  
 RA Harris J.D., Hibler D.W., Fontenot G.K., Hau K.T., Yurewicz E.C.,  
 RA Sacco A.G.;  
 RT "Cloning and characterization of zona pellucida genes and cDNAs from  
 RT a variety of mammalian species: the ZPA, ZPB and ZPC gene families";  
 RL DNA Seq. 4:361-393(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX Okazaki Y., Isojima S., Sugimoto M.;

RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ZP2 FORMS WITH ZP1 AND ZP3 THE ZONA PELLUCIDA, IN  
 CC WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.  
 CC -2- ZP2 ACTS AS A SECONDARY SPERM RECEPTOR.  
 CC -3- SUBCELLULAR LOCATION: Type 1-membrane protein. Extracellular  
 CC matrix.  
 CC -4- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES  
 CC (BY SIMILARITY).  
 CC -5- SIMILARITY: CONTAINS 1 ZP DOMAIN.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: U05776; AAA74388.1;  
 CC EMBL: D45067; BAA08095.1;  
 CC InterPro: IPR001507; Endoglin/CD105.  
 CC Pfam: PF00100; zona\_pellucida; 1.  
 CC PRINTS: PR00023; zp\_pellucida.  
 CC SMART: SM00241; ZP; 1.  
 CC PROSITE: PS00682; ZP\_DOMAIN; 1.  
 CC Glycoprotein; Signal; Sulfation; Sperm; Receptor; transmembrane;  
 CC Extracellular matrix.  
 CC SIGNAL 1 38  
 CC CHAIN 39 716 ZONA PELLUCIDA SPERM-BINDING PROTEIN 2.  
 CC DOMAIN 39 686 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 687 707 POTENTIAL.  
 CC DOMAIN 708 716 CYTOPLASMIC (POTENTIAL).  
 CC DOMAIN 369 636 ZP.  
 CC CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 222 222 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC CARBOHYD 397 397 V -> G (IN REF. 2).  
 CC CONFLICT 483 483 L -> P (IN REF. 2).  
 CC CONFLICT 637 637 F -> S (IN REF. 2).  
 CC SEQUENCE 716 AA; 80135 MW; C5745496B2CB671 CRC64;  
 CC  
 CC Query Match 5.4%; Score 82; DB 1; Length 716;  
 CC Best Local Similarity 24.5%; Pred. No. 7.1;  
 CC Matches 35; Conservative. 16; Mismatches 56; Indels 36; Gaps 7;  
 CC  
 CC 143 VFPSPKSNH-----PPFTRACDLDLPDLNACK-PFWKPNLNISQSGSDMOVS 196  
 CC 62 VEPSDFGTRKWTSVVDPFPELLNCTYILDPENLTKAPYCTRTIGQHMIRLK 121  
 CC 197 FDEAPNHEGREFYLYKLHSGFPKRTCKQSTET-----TSCLLQ-----NWSP 244  
 CC 122 -----DENASRHSLSMQLI-----NCPVMQAEFHAGSTICTKOSMSTFTFNVP 168  
 CC 245 GYIIELVDONTNTRKVMYALK 267  
 CC 169 G-----LADENTIDKMPGWSIE 186  
 CC  
 CC RESULT 10  
 CC MEC3\_CAEVU  
 CC ID MEC3\_CAEVU STANDARD; PRT; 320 AA.  
 CC AC P34765;  
 CC DT 01-FEB-1994 (Rel. 28, Created)  
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Mechanosensory protein 3.  
 CC GN MEC-3.  
 CC OS Caenorhabditis vulgaris.  
 CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 CC OC Rhabditidae; Peloderinae; Caenorhabditis.  
 CC OX NCBI\_TaxID=31233;

RR SEQUENCE FROM N.A.  
 RP MEDLINE-97084094; PubMed-1684166;  
 RX Way J.C.; Wang L.; Run J.Q.; Wang A.;  
 RA "The mec-3 gene contains cis-acting elements mediating positive and  
 RT negative regulation in cells produced by asymmetric cell division in  
 RT Caenorhabditis elegans";  
 RL Genes Dev. 5:2199-2211(1991).  
 CC -1- FUNCTION: MEC-3 SPECIES DIFFERENTIATION OF THE SET OF SIX TOUCH  
 CC RECEPTOR NEURONS. BINDS COOPERATIVELY AS A HETERODIMER WITH UNC-86  
 CC TO SITES IN THE MEC-3 GENE PROMOTER.  
 CC -2- SUBCELLULAR LOCATION: Nuclear.  
 CC -3- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
 CC -4- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
 CC IONS.  
 CC  
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 CC  
 CC EMBL: X63956; CAA45377.1;  
 CC PIR: A39479; A39479.  
 CC HSP: P06601; IFJL.  
 CC TRANSFAC: T01970;  
 CC InterPro: IPR001356; Homeobox.  
 CC InterPro: IPR001781; LIM.  
 CC Pfam: PF00046; homeobox; 1.  
 CC Pfam: PF00412; LIM; 2.  
 CC ProDom: PD000010; Homeobox; 1.  
 CC ProDom: PD000094; LIM; 2.  
 CC SMART: SM00389; HOX; 1.  
 CC SHANT: SM00132; LIM; 2.  
 CC PROSITE: PS00027; HOMEBOX\_1; FALSE\_NEG.  
 CC PROSITE: PS00071; HOMEBOX\_2; 1.  
 CC PROSITE: PS00478; LIM\_DOMAIN\_1; 2.  
 CC PROSITE: PS00233; LIM\_DOMAIN\_2; 2.  
 CC KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;  
 CC Repeat; LIM domain; Metal-binding; Zinc.  
 CC FT DOMAIN 29 79 LIM 1.  
 CC FT DOMAIN 89 145 LIM 2.  
 CC FT DNA\_BIND 216 275 HOMEBOX.  
 CC FT DOMAIN 314 320 ASP/GLU-RICH (ACIDIC).  
 CC SEQUENCE 320 AA; 36849 MW; AF98BD31C2B2PD85 CRC64;  
 CC  
 CC Query Match 5.4%; Score 81.5; DB 1; Length 320;  
 CC Best Local Similarity 31.1%; Pred. No. 2.9;  
 CC Matches 41; Conservative 9; Mismatches 47; Indels 35; Gaps 8;  
 CC  
 CC 150 NESNVHFFFTFR-----ACDLDLPDLNACK-PFWKPNLNISQSGSDMOVSDBA 200  
 CC 33 NEQIDRFYMDNHSYHCVKCTICESP--LAERKPFMKNGRYCSQ-----YTKDHS 85  
 CC 201 PENF-----GFFETLYLKLHSGFPKRTCKQSTETTTSCLL--QNVSPGDIIEVD 253  
 CC 86 SHRCAGCKGKVSPTDMVYKLKAGLVFH-----VECHCCSLGCRHLSFGQI--LVD 134  
 CC 254 DNTNTRKVM-HY 264  
 CC 135 DTMKTVSCNTHY 146  
 CC  
 CC RESULT 11  
 CC YDDB\_HAEIN  
 CC ID YDDB\_HAEIN STANDARD; PRT; 839 AA.  
 CC AC P45182;  
 CC DT 01-NOV-1995 (Rel. 32, Created)  
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Hypothetical protein H11369.









Db 107 LQESLAKELGNTYF-----LLTFPDYLPQSVMLQAPQDMGKCCGVDFVKAFAR 158  
 Qy 196 -----SFOHAPNEG-----FRFF-----YLYKLEHGP 220  
 Db 159 DSTEDKVPKSSVRLIRKVGQAFKMGPOPRABAWOFFMSDKPLHLAVLSKEIY 218  
 Qy 221 FRK -----TCKOBTFTSCLLOVNS-----PGDYIIELVDDTNTTRY 261  
 Db 219 FGEPIVTVTNNTEKTKIKALVEQVANYVLYSSDYTKFVAQETQEKV 272

Search completed: May 19, 2003, 09:20:48  
 Job time : 10.6447 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:14:29 ; Search time 21.809 Seconds

(without alignments)  
2626.495 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_36\_313

Perfect score: 1515

Sequence: 1 AUTOCORRKAARPLCVAN.....RYMYTALKPVHSPWAGPIR 278

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_muc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	788	52.0	745	13	Q8QHJ9
2	779	51.4	745	13	Q8QHJ6
3	695	45.9	582	11	Q8R5J8
4	691	45.6	564	4	Q9UFA0
5	99	6.5	341	16	Q9ZE66
6	95.5	6.3	1341	12	Q8B304
7	93	6.1	662	5	Q9UQ07
8	93	6.1	872	5	Q9U067
9	92	6.1	1428	5	Q9V003
10	91	6.0	506	10	Q94L72
11	90.5	6.0	519	13	Q9W7C2
12	89.5	5.9	368	13	Q9PW79
13	89.5	5.9	368	13	Q9IAR7
14	89.5	5.9	660	3	Q9IAR7
15	89	5.9	509	2	Q9X9S1
16	88	5.8	344	11	Q924K7

17	88	5.8	451	13	Q73719
18	88	5.8	521	13	Q9PWE8
19	88	5.8	1173	10	Q9LFR0
20	86.5	5.7	770	12	Q12935
21	86	5.7	294	12	Q89248
22	85	5.6	980	2	Q8RR74
23	83.5	5.5	278	11	Q90YL3
24	83	5.5	1121	5	Q01526
25	82.5	5.4	318	2	Q9RGV7
26	82.5	5.4	420	12	Q92487
27	82.5	5.4	461	5	Q19938
28	82.5	5.4	622	5	Q17082
29	82.5	5.4	1260	5	Q19103
30	82.5	5.4	1276	5	Q9W247
31	82	5.4	465	10	Q8VXV0
32	82	5.4	1096	13	Q90ZT1
33	82	5.4	1901	12	Q8DHE8
34	81.5	5.4	465	5	Q8T6K4
35	81	5.3	3085	5	Q97283
36	80.5	5.3	363	11	Q8R458
37	80.5	5.3	371	16	Q8CH14
38	80.5	5.3	498	10	Q9ZR09
39	80.5	5.3	538	5	Q9XVZ2
40	80.5	5.3	549	5	Q19655
41	80.5	5.3	670	16	Q8TUA8
42	80.5	5.3	501	6	Q95LS4
43	80	5.3	572	17	Q8TNJ1
44	80	5.3	2292	12	Q66850

## ALIGNMENTS

### RESULT 1

Q8QHJ9	Q8QHJ9	PRELIMINARY;	PRT; 745 AA.
ID	Q8QHJ9		
AC	Q8QHJ9;		
DT	01-JUN-2002 (TRENBLrel. 21, Created)		
DT	01-JUN-2002 (TRENBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)		
DE	Sef.		
GN	Sef.		
OC	Brachydanio rerio (zebrafish) (zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=2182436; PubMed=11802164;		
RA	Tsang W.; Friesel R.; Kudoh T.; David I.;		
RT	Identification of Sef, a novel modulator of FGF signalling.;		
RL	Nat. Cell Biol. 4:165-169(2002).		
DR	EMBL; AF364103; AAL76112.1; -		
SQ	SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DD84 CRC64;		

Query Match	52.0%	Score 788;	DB 13;	Length 745;
Best Local Similarity	53.8%;	Pred. No. 4.3e-71;		
Matches	142;	Conservative	40;	Mismatches 80;
		Indels	2;	Gaps 1;
QY	17	CYANEGVGASRNSGL--YNTFKYDNCYTLNPGVHVITADQNITISQYACHDQVAVT	74	
Db	35	CSYKQGTQSDEGRKLGIVTRINDCSYNNWPLGRKRAHEVNNITFSLSCDQAVV	94	
QY	75	ILNSPGALIEFLKFRVLEELKSGRQCQOLILNDPKOLNSFKRTGHSQPPFNKMF	134	
Db	95	VHMASPLGIEIVKGVRYLELDNPKRQCOHLILNDPKQLNFTITKMSQPPFSLAF	154	
QY	135	ETDYFKVVPFSSIKNESNYPPFFTRACDILLQPDMLACKPFWKPRNLNLSQHSQDMQ	194	
Db	155	ETDITWRIVPFFTEFLDNDFFPPFLNCSNCEVLLGPDNLCKPFWKPKLVNSQLGSLH	214	





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ID Q92566 PRELIMINARY; PRT; 341 AA.
AC Q92566
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 190 kDa antigen precursor (SCA2).
GN RP091.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E.
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,
RA Slicheritz-Ponten T., Almark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria".
RL Nature 396:133-140(1998).
DR EMBL; AJ235270; CRA14551.1;
DR InterPro; IPR003858; romPA_romPB.
DR Pfam; PF02708; romPA_romPB; 1.
RW Complete proteome.
KW Complete proteome.
SQ SEQUENCE 341 AA; 38808 MW; A43DAC317CBA42DB CRC64;

Query Match
Best Local Similarity 22.1%; Score 99; DB 16; Length 341;
Matches 69; Conservative 35; Mismatches 120; Indels 88; Gaps 15;

QY 15 RLVANEGVGPASRN-----SGLINIF-----KYDCTTILNPGKHVTAQAQ- 58
DB 52 RLKVTIVAGDEKTNVNGINISGLGVKQGWKNIPYQGRIT-----GLTIGADAEP 106
QY 59 -----NITISYACHDQVAVILNWSGALGI-EPLKGFVILIEL 97
DB 107 INNHVDVIGIAYSNEISKIYKKNLKTAVAGHLL-----SVYGLRELKGFSS--LQSI 157
QY 98 KSEGRQCOQILKDPQLNSP-FRTGSESQPLNKKFETDYFKVVPFPPSKNE-----S 152
DB 158 TSIG---HNTIKRKNLKIIGYQNNPQTLLNRYTKYINLHFTIPSIGKGYDSRAS 214
QY 153 NYHPPFTRACDLLOPN-----LACKPFKPRN--LNISQSGDMQVSEFH 199
DB 215 NYKE--TNVDIENLQKNSQSFSSIGAKIVSKPIKNNIILTSARG----- 263
QY 200 APHNPGRFFFLYHLKHEGPFKRTCKQETTTTSCILQNVSPGDYIIELVDDTNTTR 259
DB 264 ---NIERHNNKTKYNKATFKOTLQETIIPKPKLYNI--GNILMSIKINIVLL 318
QY 260 KVMHVALKPVHS 271
DB 319 EYNTTHKKYHS 330

RESULT 6
Q88304 PRELIMINARY; PRT; 1341 AA.
AC Q88304
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein precursor polypeptide.
OS Sandfly fever sicilian virus (SFS).
OC Viruses; asRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=48292;
RN [1]
RP SEQUENCE FROM N.A.
RA Glass P.J., Parker M.D.;
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U30500; AAY5043.1;
SQ SEQUENCE 1341 AA; 148766 MW; DDC6BEDEC4F9B68 CRC64;

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Query Match
Best Local Similarity 21.6%; Score 95.5; DB 12; Length 1341;
Matches 46; Conservative 25; Mismatches 65; Indels 77; Gaps 7;

QY 95 HELKSEGRQCOQILK-----DFKQLNSFRTGK-----ESQ 127
DB 433 RELMENCIOCRVORRKKPKGLLIQLADMYCOPNSTDTGPKVLGYCKYKIGNVDYRCE 482
QY 138 PFLANKKETDYFKVVPFPPSKNESNYHPPFTRACDLLOPNLACKPFKPRKPNLAIS 187
DB 483 HPASME-----EVVPEAFKNGKLYNDMSMRNKD-VLEKENFICYKAKENADASS 534
QY 188 OHSGDMQVSPDHAPHNFGFRFFLYHLKHEGPFKRTCKQETTTTSCILQNVSPGDY 247
DB 535 NRGGRKVSF-----KYTEC--KNYDPSQN 555
QY 248 IIELVDDTNTTRKVMHYALKPVH---SPWAGPI 277
DB 556 KICSGDNTFCFACHNELPEVHCEVAPGAGPI 588

RESULT 7.
Q9UAQ7 PRELIMINARY; PRT; 662 AA.
AC Q9UAQ7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 75.8 kDa protein.
GN C39P7.5
OS Caenorhabditis elegans
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Scheet P., Maggi L., Dubbelde C.;
RT "The sequence of C. elegans cosmid C39P7."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RT "Direct Submission."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF101310; AAC69214.2;
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR000345; CytC_heme_bind.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 662 AA; 75799 MW; DD64BBCA0579E102 CRC64;

Query Match
Best Local Similarity 23.4%; Score 93; DB 5; Length 662;
Matches 51; Conservative 24; Mismatches 65; Indels 78; Gaps 10;

QY 101 GRCQCOQILKDPQLNSFKR---TGMSQPF-----LNK---KFETDYFKV 143
DB 26 GILSARNVLAATSLKFKSRKSTRQIRPFELIKSWPVQDLNLLAEFAD--SKLL 83
QY 144 FPPSIKNESNYHPPFTRACDLLOPNLACKPFKPR---NLNI----- 186

```



Db 259 NGGNDPQIAFFITLQAGCTPFFTHKDFNGSHTSYILDHFKNTFFYLRIKNGKNSGNG 318  
 QY 58 -----ONITISQACHOV-----AVTILSPGALG-IEFLKGFVILEEL 97  
 Db 319 OPTOYPOGIIITLSI--DPIPEKVEFTGSTATTIGMPPPPDLIDYIOYELIYSE- 374  
 QY 98 KSGRQCQOILIKDKQLNSFKRTGSEOPFLNKKFETDIFVKVVPFSSIKNESYHPF 157  
 Db 375 --SG-----EVPKVEEAIYQONSRLPYN-----FDKLTATDYE-- 408  
 QY 158 FFRTRACDILLQDNLACKPFW-----KPRMLNISQR-----GSDMOVSF 197  
 Db 409 -FRVACSLQTK--TCGP-WSENVNGTMDGVATKFTNLSIOCHDHNVTNGSIALNW 462  
 QY 198 DHAPENFGFRFFLYHLKKGEPKRTK-----KQSTTETTSCLLQNVSPGDIY 249  
 Db 463 D-VKTPNGKTL-----ESVSPNTNTVTVSAITRUKKNGEPATGSLMPVSTPDAIGR 516  
 QY 250 ELVNDRTNTRKVMYALK---PVHSPWAGPI-277  
 Db 517 TMSKVNLSK---IVLKLYLPKISERNGPI 544

RESULT 10  
 Q94/LT2 PRELIMINARY; PRT; 506 AA.

AC Q94/LT2  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Hypothetical 56.6 kDa protein.  
 OS Oryza sativa (Rice)  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Ehrhartoideae; Oryzoaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CV. NIPPONBARE;  
 RA Buell C.R., Yuan G., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,  
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,  
 RA Riggs F., Siao J., Zismann V., Blunt S., Pai G., VanAken S.E.,  
 RA Utterback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,  
 RA White O., Fraser C.M.;  
 RT "Oryza sativa chromosome 10 BAC OSJNB0011A08 genomic sequence."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EXBL; AC034258; AAK54291.1;  
 DR InterPro: IPR004263; Exostosin.  
 DR Pfam: PF03016; Exostosin; 1.  
 KN Hypothetical protein.  
 SQ SEQUENCE 506 AA; 56612 MW; B35878D1F1CE24CE CRC64;

Query Match 6.0%; Score 91; DB 10; Length 506;  
 Best Local Similarity 20.8%; Pred. No. 1.3;  
 Matches 60; Conservative 34; Mismatches 82; Indels 112; Gaps 14;

QY 18 VANEVGVPASRNSGLNITFYKDYCNCTYLNPGVGHVIAADNAQNTISQYAC--HQDAVTI 75  
 Db 113 VVNDGFGPALGGGALPERDYD-----TDQYMLAIYHARNRYECLTGDAADA 164  
 QY 76 LWSFGALGTEFLKGFVILELASE-----GRCOOLIKDKPKQLNS----- 117  
 Db 165 VTFP-----FYAGDAAMLMKSDLAARDALPQLAEVLRPEWRWANGGRDHFNVAAR 218  
 QY 118 -----SFRFG-----MESQFLMKFETDYFVKVFPFSSIKNESN 153  
 Db 219 FVNDYFRGGDGGWGNALLTPAIRNTVLTVEANPWRGIDFG-----VDFP-----SH 266  
 QY 154 YHPFFRTACDILLQDNLACKPFWKPNLNISQHGSDMQVSDHAPENFGFRFFLYHY 213  
 Db 267 FHP-----TSADVLR-----WQDR---MRRGRRLWMAFAGAPR----- 298  
 QY 214 KLKHEGFFPKRTCKQ---EQFTTETTSCLLQNVSPGDI-----IIELV 253

Db 299 -----PGSTKTVRAQIEQCTASPSCTHFSGSGHYNSPGRINELLE 340

RESULT 11  
 Q9W7C2 PRELIMINARY; PRT; 519 AA.

AC Q9W7C2  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE T-box transcription factor Tbx5.  
 GN TBX5  
 OS Xenopus laevis (African clawed frog)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99180578; PubMed-10079235;  
 RA Horb M.E., Thomsen G.E.;  
 RT "Tbx5 is essential for heart development."  
 RL Development 126:1739-1751(1999).  
 DR EMBL; AF133036; AAD23592.1;  
 DR HSP; P24781; IYBR.  
 DR TRANSFAC; T04422;  
 DR InterPro: IPR001699; TF\_T-box.  
 DR Pfam: PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00435; TBOX; 1.  
 DR PROSITE; PS01288; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS0252; TBOX\_3; 1.  
 SQ SEQUENCE 519 AA; 58080 MW; 8B5E096C67FC3D1E CRC64;

Query Match 6.0%; Score 90.5; DB 13; Length 519;  
 Best Local Similarity 20.9%; Pred. No. 1.5;  
 Matches 61; Conservative 42; Mismatches 90; Indels 99; Gaps 15;

QY 13 RPLRCV--ANGGVGPASRNSGLNITFYKDYCNCTYLNPGVGHVIAADNAQNTISQYACHQ 70  
 Db 180 QPRLHVRADENNGGSKNTAF-----CT-----HVESETDFIAVTSYONHKI 222  
 QY 71 VAVTILSPGALGTEFLKGFVILELASEGRCOOLIKDKPKQLNSFKRTGSEOPFL 130  
 Db 223 TQLAKIENP-----PAKFRG-----SDDELEH---RMSRQSKLEY- 255  
 QY 131 NMKFEIDFVKVVPFSPSIKNE--SNYHPFFPFR-----ACDILL 167  
 Db 256 -----PVPFRSTVRKVSNNHSPFSQETRNITGSTLNLSYOCENGVSTSQDLL 305  
 QY 168 LQDNLACKPFWKPNLNISQHGSDMQVSDHAPENFGFRFFLYHLKHEGFFPKRTCK 227  
 Db 306 --PSSSAVTSL--PHESGTIYHCTKATVSEPAHS--YKAPYMDTSPSEDPFYSRGP 359  
 QY 228 Q--EQTTETS-----CLLQNVSPGDIIELVDD--TNTTRKVMHYA 265  
 Db 360 QPSSSSSTTSFRFESAQRQACHASSAPATPEVPSIEDISCSNHSSTVPSIS 411

RESULT 12  
 Q9PW79 PRELIMINARY; PRT; 368 AA.

AC Q9PW79  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 GN TVB3.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

```

DR Pfam: PF00020; TNFR_C6; 2.  

DR SMART: SM00005; DEATH; 1.  

DR SMART: SM00208; TNFR; 2.  

DR PROSITE: PS00198; 4FEAS_FERREDOXIN; UNKNOWN_1.  

DR PROSITE: PS0017; DEATH_DOMAIN; 1.  

DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.  

DR PROSITE: PS0050; TNFR_NGFR_2; 2.  

DR PROSITE: PS0050; TNFR_NGFR_2; 2.  

DR SEQ SEQUENCE 368 AA; 41531 MW; 0553CE51DDEB47C6 CRC64;  

  

Query Match          5.9%; Score 89.5; DB 13; Length 368;  

Best Local Similarity 22.9%; Pred. No. 1.2;  

Matches 36; Conservative 19; Mismatches 49; Indels 53; Gaps  

  

QY 77 WSPGANGIEFLKGFVILEELKSEGRCQQILIKDPQLMNSFKRGHESOPFLNM-----132  

DB 195 WKPSAV-----VNRLRLRIGTDNRCHEDYLQRQQOELLFTAGSEVPGVEMGE 247  

  

QY 133 -----KFET-----DFVKVPFPFSIKNSENHPFFETRAD- 165  

DB 248 RRTPDPEVTQRKVLPVLGENPITALLHRSFNTFYDYPPFMRFG-----RALDL 298  

  

QY 166 -----LLQPONLACKPFWKPRNLNLSIQSGSDMQVS 196  

DB 299 QENDLYLAEOHDVRVSCPEPYOMLTNTWLNOOGSKASVN 335  

  

RESULT 14  

QCCLM9 PRELIMINARY; PRT: 660 AA.  

ID QCCLM9  

AC QCCLM9  

DT 01-JUN-2001 (TREMBLrel. 17, Created)  

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  

GN Alpha-L-rhamnosidase A precursor (EC 3.2.1.40).  

GN RHAA.  

OS Aspergillus aculeatus.  

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  

OX Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  

NCBI_TaxId=5053;  

RN [1]  

RP MEDLINE; Pubmed=11319105;  

RX Manzanares P., van den Broeck H.C., de Graaff L.H., Visser J.;  

RT "Purification and Characterization of Two Different alpha-L-  

RT Rhamnosidases, RhAa and RhAb, from Aspergillus aculeatus";  

RL Appl. Environ. Microbiol. 67:2230-2234(2001).  

BL EMBL; AF284761; AAA16249.1;  

KW Glycosylase; Hydrolase; Signal.  

FT SIGNAL 1 19 POTENTIAL.  

SQ SEQUENCE 660 AA; 71218 MW; A550A9F4D0E42984 CRC64;  

  

Query Match          5.9%; Score 89.5; DB 3; Length 660;  

Best Local Similarity 22.4%; Pred. No. 2.6;  

Matches 57; Conservative 29; Mismatches 92; Indels 77; Gaps  

  

QY 3 TCGRWKAARPLCVANEGVGPAISNSGLNITFKYDNCTYYLNPVGKHVIADAQNITI 2  

DB 403 TAASKIAANAARLWA-----ONSLEY-----DNETTTLPDGNAWAKANLTL 448  

  

QY 63 SQYACIED-QVANTILWSP-----GALGTEFLKGFRVILLEKSEGRCQQILI-----108  

DB 449 SSNGSRAISSALAARWGYPAPAEAGSVTSPTGGFELQAHLANEFDRLDLLRLQWG 508  

  

QY 109 --LNDPKQINSFKTKGHESOPFLNMKKFTDYFKVVVPFPFSIKNSENTH-----PFFFFT 161  

DB 509 FMDDPRMTNSTF-----IEG-----YSTDGSLAYAPTENTPVSHAGWGSTGTSAULT 557  

  

QY 162 R-----ACDLLQPDNLACKPFWKPRNLNLSIQSGSDMQVSFDEAPHNPGFRFFT 210  

DB 558 HYTAGLRLLTGPAGSTWLFKP-----QPGNLTEVOAQGETOLG-----LEA 597  

  

QY 211 LHKLKHEGPFRKKT 225
```





GenCore version 5.1.4 ps\_1578  
Copyright (c) 1993-2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 09:07:58 ; Search time 54.0074 seconds  
(without alignments)  
1771.498 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_36\_753

Perfect score: 3829

Sequence: 1 ADTCGWRKAAARPLCVAN.....CAALGCRSVTDELAVALP 718

Scoring table: BLOSUM62

Gapop 10.0 - Gapart 0.5

Searched: 908470 seqs, 133250620 residues.

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq.101002.\*

ID	Seq	Length	DB	ID	Seq	Length	DB
1	/SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*	753	23	ABB07626	Human cytokine rec	753	23
2	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*	753	23	ABB07627	Human cytokine rec	753	23
3	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*	753	23	ABB07628	Human cytokine rec	753	23
4	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*	753	23	AAU09904	Human interleukin	738	22
5	/SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*	753	23	AAU09905	Human interleukin	738	22
6	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*	753	23	AAU09954	Human interleukin	738	22
7	/SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*	753	23	AAU09955	Human interleukin	738	22
8	/SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*	753	23	AAU09956	Human interleukin	738	22
9	/SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*	753	23	AAU09955	Human interleukin	738	22
10	/SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*	753	23				
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12	/SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*	753	23				
13	/SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*	753	23				
14	/SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*	753	23				
15	/SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*	753	23				
16	/SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*	753	23				
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18	/SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*	753	23				
19	/SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*	753	23				
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21	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*	753	23				
22	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*	753	23				
23	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*	753	23				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3829	100.0	753	23	ABB07626
2	3819	99.7	753	23	ABB07627
3	3741	97.7	739	23	ABB07628
4	3725	97.3	738	22	AAU09904
5	3721	97.2	738	22	AAU09905
6	3720	97.2	738	22	AAU09954
7	3718	97.1	738	22	AAU09955
8	3718	97.1	738	22	AAU09956
9	3718	97.1	738	22	AAU09955
10	3714	97.0	738	22	AAU09955

11	3714	97.0	738	22	AAU09957	Human Interleukin
12	3703	96.7	738	22	AAU04958	Human Interleukin
13	3700	96.6	739	22	AAU10602	Human Interleukin
14	3657.5	95.5	738	23	AAU11355	Human DNA cytokine
15	3208	83.8	739	23	ABB07630	Murine cytokine re
16	2515.5	65.7	554	23	AAU91330	Human novel secret
17	1334	34.8	296	22	AAU10601	Human interleukin-5' portion of Huma
18	312	8.1	866	17	AAU04185	Human interleukin-
19	312	8.1	866	19	AAU61272	Human interleukin-
20	312	8.1	866	20	AAU2409	Human IL-17R prote
21	312	8.1	866	21	AAU99941	Human interleukin-
22	312	8.1	866	21	AAU97131	Human interleukin-
23	312	8.1	866	21	AAU97181	Human interleukin-
24	312	8.1	866	21	AAU03807	Human interleukin-
25	312	8.1	866	22	AAU62066	Human IL-17R (bCTL
26	312	8.1	866	22	AAU72754	Human Interleukin-
27	306	8.0	864	17	AAU04184	Murine interleukin
28	306	8.0	864	19	AAU61271	Mouse interleukin
29	306	8.0	864	20	AAU2408	Murine IL-17R prot
30	306	8.0	864	21	AAU99933	Murine IL-17R prot
31	306	8.0	864	21	AAU97130	Murine interleukin
32	306	8.0	864	21	AAU97180	Murine interleukin
33	306	8.0	864	21	AAU03806	Murine interleukin
34	306	8.0	864	22	AAU62060	Murine IL-17R poly
35	306	8.0	864	22	AAU72748	Murine Interleukin
36	271.5	7.1	539	23	AAU47457	Human IL-17 recept
37	135.5	3.5	238	20	AAU31624	Human IL-17RH matu
38	135.5	3.5	385	21	AAU25795	Human secreted pro
39	135.5	3.5	385	22	AAU75381	Human secreted pro
40	135.5	3.5	385	23	AAU47459	Human IL-17 recept
41	135.5	3.5	502	22	AAU29233	Human PRO polypept
42	135.5	3.5	502	22	AAU24349	Human EST encoded
43	135.5	3.5	502	22	AAU04955	Human Interleukin
44	135.5	3.5	502	22	AAU06586	Human protein havi
45	135.5	3.5	502	22	AAU87604	Human PRO5801. RO

#### ALIGNMENTS

RESULT 1  
ABB07626  
ID ABB07626 standard; Protein; 753 aa.

AC ABB07626;

XX ABB07626;

XX 20-MAY-2002 (first entry)

DE Human cytokine receptor, zcytor18 amino acid sequence.

XX Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;

XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;

XX erythroleukemia; chromosome 3p14.3; gene therapy.

XX Homo sapiens.

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23253.

XX 26-JUL-2000; 2000US-220747P.

XX (SYM) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/77.

XX N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for

XX inhibiting cell proliferation associated with psoriasis or tumor

PT growth, and modulating immune system by binding to endogenous zcytor18.  
 PT ligand.  
 XX Claim 1; Page 2; 119pp; English.  
 XX The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumour growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 amino acid sequence.  
 XX Sequence 753 AA;  
 SQ  
 Query Match 100.0%; Score 3829; DB 23; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADTCGWRKAAARPRCLVANGVGPASRNSGLNITFKYDNCNTTYLNPVKGKVIADAQNI 60  
 DB 36 ADTCGWRKAAARPRCLVANGVGPASRNSGLNITFKYDNCNTTYLNPVKGKVIADAQNI 95  
 QY 61 TTSOACHQDVAVTILMSGALGIEFLRGFVILEELKSGRQCOQLIKDPQLNSPFK 120  
 DB 96 TTSOACHQDVAVTILMSGALGIEFLRGFVILEELKSGRQCOQLIKDPQLNSPFK 155  
 QY 121 RTGMSQPLNKKFTDYFVKVVPFSPKSNYHFFTRACDLILQPDNLACKPFWK 180  
 DB 156 RTGMSQPLNKKFTDYFVKVVPFSPKSNYHFFTRACDLILQPDNLACKPFWK 215  
 QY 181 PRNLISQSGDMQVDFDAPNFGFEPFLYKLKHEGPFKRTCKOBTETTSCILQ 240  
 DB 216 PRNLISQSGDMQVDFDAPNFGFEPFLYKLKHEGPFKRTCKOBTETTSCILQ 275  
 QY 241 NVSPGDIYIELVDNTTRVHYALKPVSAGPIRAVATVPLVWISAPATLTVNC 300  
 DB 276 NVSPGDIYIELVDNTTRVHYALKPVSAGPIRAVATVPLVWISAPATLTVNC 335  
 QY 301 RKQOENIYSHLDESESTTAAALPRRLPRPKVFCYSSKDGQGNHNVVQCFAYEL 360  
 DB 336 RKQOENIYSHLDESESTTAAALPRRLPRPKVFCYSSKDGQGNHNVVQCFAYEL 395  
 QY 361 QDFCCEVALDMEFSLCREGREWVTKIHESQFIIVVCSKGMKVFVDKKNYKKGSG 420  
 DB 396 QDFCCEVALDMEFSLCREGREWVTKIHESQFIIVVCSKGMKVFVDKKNYKKGSG 455  
 QY 421 RSGSGELFLVAVSATAKRLQAKSSAALSKFIATVFDYSCSDVPGILDLSTYRLM 480  
 DB 456 RSGSGELFLVAVSATAKRLQAKSSAALSKFIATVFDYSCSDVPGILDLSTYRLM 515  
 QY 481 DMLPOLCSHLSDHGLQPCQHTQGSRRNFRSKGSLYVACNNHQFIDEEPDPFE 540  
 DB 516 DMLPOLCSHLSDHGLQPCQHTQGSRRNFRSKGSLYVACNNHQFIDEEPDPFE 575  
 QY 541 KQVFPPFPPLRYREPVLEKFDGSLVLDVYMKCPGPEDFCLKVEAAVLTGATPADSOHE 600  
 DB 576 KQVFPPFPPLRYREPVLEKFDGSLVLDVYMKCPGPEDFCLKVEAAVLTGATPADSOHE 635  
 QY 601 SQHGLDQDCEARPDALDQSAALQPLHTVKGSPDMRDSGIYDSSVPSSLSLPLEG 660  
 DB 636 SQHGLDQDCEARPDALDQSAALQPLHTVKGSPDMRDSGIYDSSVPSSLSLPLEG 695  
 QY 661 LSTQDTETSSITSSVSSSGLEEPALPSKLLSGSGCKADLCGRSYTDELHVAVPL 718  
 DB 696 LSTQDTETSSITSSVSSSGLEEPALPSKLLSGSGCKADLCGRSYTDELHVAVPL 753

## RESULT 2

AB807627  
 ID: AB807627 standard; Protein; 753 AA.

XX AC AB807627;

XX DT 20-MAY-2002 (first entry)

XX DE Human cytokine receptor, zcytor18 variant sequence.

XX KW Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
 XX KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;  
 XX KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 269

XX FT /label- T369M /note- "wild-type Thr is replaced with Met"

XX FT Misc-difference 750

XX FT /label- V750A /note- "wild-type Val is replaced with Ala"

XX FT

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QY 61 TISQACHQDVAVTILKSPGALGTEFLKGRVILKELSGRQCOOLILKPKQLNSFK 120  
 DB TISQACHQDVAVTILKSPGALGTEFLKGRVILKELSGRQCOOLILKPKQLNSFK 155  
 QY 121 RTGMSQPLNKKFTDTFVKVVPFSSIKNESNYHFFRFRACDILLODKLACKFWK 180  
 DB RTGMSQPLNKKFTDTFVKVVPFSSIKNESNYHFFRFRACDILLODKLACKFWK 215  
 QY 181 PRNLISQSGDMQVSDHAPNHFGRFFLYLKLKHEGPKFKTKQQTETTSCLLQ 240  
 DB PRNLISQSGDMQVSDHAPNHFGRFFLYLKLKHEGPKFKTKQQTETTSCLLQ 275  
 QY 241 NVSPGDIIELVDDNTTKVMYHVALKPVHSPWAGPIRAVAITVPLVWISAFATLVMC 300  
 DB NVSPGDIIELVDDNTTKVMYHVALKPVHSPWAGPIRAVAITVPLVWISAFATLVMC 335  
 QY 301 RKQOENIYSHLDESSSTYTAALPRERLRPRKVKFLCYSSKQGNHNNVVOCFATFL 360  
 DB RKQOENIYSHLDESSSTYTAALPRERLRPRKVKFLCYSSKQGNHNNVVOCFATFL 395  
 QY 361 QDFCGEVALDWEFSLCRQRENIQIHESQFIIVVCSKGMKVFYDKNKHKG 420  
 DB QDFCGEVALDWEFSLCRQRENIQIHESQFIIVVCSKGMKVFYDKNKHKG 455  
 QY 421 RGSQGELELVAVSAIAELKRAQKSSAALSFKPIANTFYDSCBQVPGILDSTKRLM 480  
 DB RGSQGELELVAVSAIAELKRAQKSSAALSFKPIANTFYDSCBQVPGILDSTKRLM 515  
 QY 481 DNLPGCSHLHSDRGLOEPQCHTROGSRNFRSKGRSLYVAICNMQHOFIDEPDWE 540  
 DB DNLPGCSHLHSDRGLOEPQCHTROGSRNFRSKGRSLYVAICNMQHOFIDEPDWE 575  
 QY 541 KQVFPFPPPLATREPVLEKFDGLVNDVCMKPGPESDFCLKVEAAVLGATGPDQSHE 600  
 DB KQVFPFPPPLATREPVLEKFDGLVNDVCMKPGPESDFCLKVEAAVLGATGPDQSHE 635  
 QY 601 SOHGLDQDGEARPAIDGSAALQPLLTHTVKGSPDMPSGDIYSSVSSLSPLMEG 660  
 DB SOHGLDQDGEARPAIDGSAALQPLLTHTVKGSPDMPSGDIYSSVSSLSPLMEG 695  
 QY 661 LSTDTTSLTSVSSSGGEEPPALPSPHLLSGSCRADLGCRSTDELHVAAPL 718  
 DB LSTDTTSLTSVSSSGGEEPPALPSPHLLSGSCRADLGCRSTDELHVAAPL 753

RESULT 3  
 ABB07628  
 ID ABB07628 standard; Protein: 739 AA.

AC ABB07628;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, zcytor18 splice variant.

KW Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;  
 KW Pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

OS Homo sapiens.

PN WO200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-US33253.

PR 26-JUL-2000; 2000US-220747P.

PA (2MO) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

DR WPI: 2002-217048/27  
 DR N-PSDB; ABA95035; ABA95036.  
 PT New cytokine receptor polypeptide designated zcytor18, useful for  
 PT inhibiting cell proliferation associated with psoriasis or tumor  
 PT growth, and modulating immune system by binding to endogenous zcytor18  
 PT ligand  
 XX  
 PS Claim 1; Page 102-106; 119pp; English.  
 CC The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumor growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo for gene  
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 splice variant.

XX Sequence 739 AA;

Query Match 97.7%; Score 3741; DB 23; Length 739;  
 Best Local Similarity 98.1%; Pred. No. 0;  
 Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 ADTCGRNRKAAARPLCVANEGVGPASRNSGLNITFKYDNCNTYLPVGRVIAADQNI 60  
 DB 36 ADTCGRNRKAAARPLCVANEGVGPASRNSGLNITFKYDNCNTYLPVGRVIAADQNI 81  
 QY 61 TISQACHQDVAVTILKSPGALGTEFLKGRVILKELSGRQCOOLILKPKQLNSFK 120  
 DB 82 TISQACHQDVAVTILKSPGALGTEFLKGRVILKELSGRQCOOLILKPKQLNSFK 141  
 QY 121 RTGMSQPLNKKFTDTFVKVVPFSSIKNESNYHFFRFRACDILLODKLACKFWK 180  
 DB 142 RTGMSQPLNKKFTDTFVKVVPFSSIKNESNYHFFRFRACDILLODKLACKFWK 201  
 QY 181 PRNLISQSGDMQVSDHAPNHFGRFFLYLKLKHEGPKFKTKQQTETTSCLLQ 240  
 DB 202 PRNLISQSGDMQVSDHAPNHFGRFFLYLKLKHEGPKFKTKQQTETTSCLLQ 261  
 QY 241 NVSPGDIIELVDDNTTKVMYHVALKPVHSPWAGPIRAVAITVPLVWISAFATLVMC 300  
 DB 262 NVSPGDIIELVDDNTTKVMYHVALKPVHSPWAGPIRAVAITVPLVWISAFATLVMC 321  
 QY 301 RKQOENIYSHLDESSSTYTAALPRERLRPRKVKFLCYSSKQGNHNNVVOCFATFL 360  
 DB 322 RKQOENIYSHLDESSSTYTAALPRERLRPRKVKFLCYSSKQGNHNNVVOCFATFL 381  
 QY 361 QDFCGEVALDWEFSLCRQRENIQIHESQFIIVVCSKGMKVFYDKNKHKG 420  
 DB 382 QDFCGEVALDWEFSLCRQRENIQIHESQFIIVVCSKGMKVFYDKNKHKG 441  
 QY 421 RGSQGELELVAVSAIAELKRAQKSSAALSFKPIANTFYDSCBQVPGILDSTKRLM 480  
 DB 442 RGSQGELELVAVSAIAELKRAQKSSAALSFKPIANTFYDSCBQVPGILDSTKRLM 501  
 QY 481 DNLPGCSHLHSDRGLOEPQCHTROGSRNFRSKGRSLYVAICNMQHOFIDEPDWE 540  
 DB 502 DNLPGCSHLHSDRGLOEPQCHTROGSRNFRSKGRSLYVAICNMQHOFIDEPDWE 561  
 QY 541 KQVFPFPPPLATREPVLEKFDGLVNDVCMKPGPESDFCLKVEAAVLGATGPDQSHE 600  
 DB 562 KQVFPFPPPLATREPVLEKFDGLVNDVCMKPGPESDFCLKVEAAVLGATGPDQSHE 621  
 QY 601 SOHGLDQDGEARPAIDGSAALQPLLTHTVKGSPDMPSGDIYSSVSSLSPLMEG 660

Db 622 SQBGLDQGEARALDGSAAALQPILETVTRAGSPDNRDSDGTYDSSVPSSELSPLMBG 681  
 Qy 661 LSTDOTETSSITSSVSSSGGEEPPALPKLLSSGCKADLCGRSTYDELHNAVPL 718  
 Db 682 LSTDOTETSSITSSVSSSGGEEPPALPKLLSSGCKADLCGRSTYDELHNAVPL 739

## RESULT 4

AAU09904  
 ID AAU09904 standard; Protein; 738 AA.

XX AC AAU09904;

XX DT 14-FEB-2002 (first entry)

XX DB Human Interleukin 17 (hIL-17) receptor like protein.

XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human.

XX OS Homo sapiens.

XX PN W020016899-A2.

XX PD 20-SEP-2001.

XX PF 15-MAR-2001; 2001WO-US08678.

XX PR 16-MAR-2000; 2000US-189816P.

XX PS 28-NOV-2000; 2000US-0724460.

XX PA (AMGE-) AMGEN INC.

XX PI Jing S;

XX WPL: 2001-611392/70.

XX N-PSDB; RAS15346.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma.

XX Claim 2; Page 152-154; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (hIL17) expression. These  
 XX include, for example immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infections (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of smaller nucleic acids in samples and identify  
 XX patients needing restorative therapy. The hIL17 may also be used as  
 XX antigens in the production of antibodies against the proteins and in  
 XX assays to identify modulators of expression and activity. The

CC anti-IL17p antibodies and antagonists may also be used to down regulate  
 CC expression and activity. This is the amino acid sequence of the human  
 CC Interleukin 17 (IL-17) receptor like protein described in the method of  
 CC the invention.  
 XX  
 XX Sequence 738 AA;

Query Match 97.38; Score 3725; DB 22; Length 738;  
 Best Local Similarity 97.8%; Pred. No. 0;  
 Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTGWRKAAARPLCAVNEGVPASRNSGLYITFKYDNCTTYINPVGSHVIAQAQNT 61

Db 37 DTGWR-----GVGPASRNSGLYITFKYDNCTTYINPVGSHVIAQAQNT 82

Qy 62 ISOYACHDOAVVILWSPGALGIEFLAGFVILEELKSGRCOOLIKDPQLNSSFRR 121

Db 83 ISOYACHDOAVVILWSPGALGIEFLAGFVILEELKSGRCOOLIKDPQLNSSFRR 142

Qy 122 TGMSSQPLNKKETDYFKVVPSPSKNESNTHPEFTTRACDLLOPNLACKPFPKP 181

Db 143 TGMSSQPLNKKETDYFKVVPSPSKNESNTHPEFTTRACDLLOPNLACKPFPKP 202

Qy 182 RMLNISQSGSDMVSDHAPHNFRFTLYHKLHSGPFRKTKCKOQTETTSCLLN 241

Db 203 RMLNISQSGSDMVSDHAPHNFRFTLYHKLHSGPFRKTKCKOQTETTSCLLN 262

Qy 242 VSPGDYIIELVDDTNTTRKVMHYALAKPVHSPAGPIRAVAITVPLVVISAFATLTVACR 301

Db 263 VSPGDYIIELVDDTNTTRKVMHYALAKPVHSPAGPIRAVAITVPLVVISAFATLTVACR 322

Qy 302 KKOENIYSHLDESSESSTYTAALPRERLRPRKPVFLCTSSKDGQHNHNVVQCFAFLQ 361

Db 323 KKOENIYSHLDESSESSTYTAALPRERLRPRKPVFLCTSSKDGQHNHNVVQCFAFLQ 382

Qy 362 DFCGCEVALDLEDFSLCREGSEWVTKHESOFIIVVCSKGNKVFVDKKNYKKGGR 421

Db 383 DFCGCEVALDLEDFSLCREGSEWVTKHESOFIIVVCSKGNKVFVDKKNYKKGGR 442

Qy 422 GSGKGLFLVAVSAIAEKLRKONKSSAALSKFIATVFDYCEGDVGIIDLTSTYRLMD 481

Db 443 GSGKGLFLVAVSAIAEKLRKONKSSAALSKFIATVFDYCEGDVGIIDLTSTYRLMD 502

Qy 482 NLPLQCSHLASRDHGLQEPQHTROGSRNNYFRSKSGSLVVAICNNHOFIDEEPDMFEK 541

Db 503 NLPLQCSHLASRDHGLQEPQHTROGSRNNYFRSKSGSLVVAICNNHOFIDEEPDMFEK 562

Qy 542 QFVPPHPPLRTPEPVLKDFSGVLVNDVMCKRPGSPDFCLKVEAAVLGATGPADSQHES 601

Db 563 QFVPPHPPLRTPEPVLKDFSGVLVNDVMCKRPGSPDFCLKVEAPVLGATGPADSQHES 622

Qy 602 QHGLDQGEARALDGSAAALQPILETVTRAGSPDNRDSDGTYDSSVPSSELSPLMBGL 661

Db 623 QHGLDQGEARALDGSAAALQPILETVTRAGSPDNRDSDGTYDSSVPSSELSPLMBGL 682

Qy 662 STDQETSSITSSVSSSGGEEPPALPKLLSSGCKADLCGRSTYDELHNAVAP 717

Db 683 STDQETSSITSSVSSSGGEEPPALPKLLSSGCKADLCGRSTYDELHNAVAP 738

## RESULT 5

AAU09953

ID AAU09953 standard; Protein; 738 AA.

XX AC AAU09953;

XX DT 14-FEB-2002 (first entry)

XX DB Human Interleukin 17 (hIL-17) receptor like protein substitution #3.

XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;

XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;

anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human; mutant; mutin  
Homo sapiens  
Synthetic

Key Location/Qualifiers

Misc-difference 363 /label= Ser, Thr, Ala, Cys

W0200168859-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-0508678.

16-MAR-2000; 2000US-189816P.

28-NOV-2000; 2000US-0724460.

(AMGE-) ANGEN INC.

Jing S.

WPI, 2001-611392/70.

Nucleic acids encoding Interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma  
Claim 20; Page 7; 158pp; English.

The invention describes novel nucleic acids encoding Interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17R) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17R may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17R antibodies and antagonists may also be used to down regulate expression and activity.  
Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09954) and has been created according to information given in claim 20.

Sequence 738 AA;

Query Match 97.24; Score 3721; DB 22; Length 738;  
Best Local Similarity 97.64; Pred. No. 0;  
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;  
OY 2 DTCGRRMKAARPLCVANEGVGPASRRNSGLNITFKYDNCNTYTLNPGKHVIADANQIT 61  
Db 37 DTCGRR-----GVGPASRRNSGLNITFKYDNCNTYTLNPGKHVIADANQIT 82

62 ISYACHDOAVATILSPALGIEFLKGPVILFELKSGRCOOLILKPKOLNSPER 121  
Db 83 ISYACHDOAVATILSPALGIEFLKGPVILFELKSGRCOOLILKPKOLNSPER 142  
OY 122 TCHESQPLANKFETIDYFKVVPFPPS IANESNTHPPFFTRACDILLLOPNLACKPFWKP 181  
Db 143 TCHESQPLANKFETIDYFKVVPFPPS IANESNTHPPFFTRACDILLLOPNLACKPFWKP 202  
OY 182 RNLTNSQSGDMQVDFHAPNFGFRFFLYLKLKEGPFKRTCKQEQTTTSCLLQ 241  
Db 203 RNLTNSQSGDMQVDFHAPNFGFRFFLYLKLKEGPFKRTCKQEQTTTSCLLQ 262  
OY 242 VSPGYIIELVDDTNTTRVNYALKPVHSPWAGPIRAVAITVPLWISAPATLPTVWCR 301  
Db 263 VSPGYIIELVDDTNTTRVNYALKPVHSPWAGPIRAVAITVPLWISAPATLPTVWCR 322  
OY 302 KIQENIYSHLDESSSTYTAALPRELPPRPVPLCYSSDQGNHNVVOCFAFLQ 361  
Db 323 KIQENIYSHLDESSSTYTAALPRELPPRPVPLCYSSDQGNHNVVOCFAFLQ 382  
OY 362 DFCGCEVALDMEFSLCREGOREWVIOKIHESQFIIVVCSGKMYFVDKNTKHGGGR 421  
Db 383 DFCGCEVALDMEFSLCREGOREWVIOKIHESQFIIVVCSGKMYFVDKNTKHGGGR 442  
OY 422 GSGKGEFLVAVSAIAEKLRQAKSSAALSRTIAYTFDYSCGDFVGLDLSKRYLMD 481  
Db 443 GSGKGEFLVAVSAIAEKLRQAKSSAALSRTIAYTFDYSCGDFVGLDLSKRYLMD 502  
OY 482 NLPOLCSHLSRDRGLQEPQHTROGSRRTYFKSGRSLYVAICNMHOFIDEEPWFKE 541  
Db 503 NLPOLCSHLSRDRGLQEPQHTROGSRRTYFKSGRSLYVAICNMHOFIDEEPWFKE 562  
OY 542 QVVPHPPLPYEPLVLEKFDGSLVNDVCKPESDPCLVAVLGAATGADSDHES 601  
Db 563 QVVPHPPLPYEPLVLEKFDGSLVNDVCKPESDPCLVAVLGAATGADSDHES 622  
OY 602 QIGGLDQGEARPALDGSAAQLPILHTVAGSDMPDRSGITDSSVPSSELSLPLMBGL 661  
Db 623 QIGGLDQGEARPALDGSAAQLPILHTVAGSDMPDRSGITDSSVPSSELSLPLMBGL 682  
OY 662 STDQETSSSTESVSSSGGLGEEPPALPSKLLSSGCKADIGCRSYTDELHAVAP 717  
Db 683 STDQETSSSTESVSSSGGLGEEPPALPSKLLSSGCKADIGCRSYTDELHAVAP 738

RESULT 6

AAU09954

ID AAU09954 standard; Protein; 738 AA.

XX AAU09954;

XX AAU09954;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #4.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
XX autelin.

OS Homo sapiens.

OS Synthetic.

XX Key

XX Location/Qualifiers

FT Misc-difference 374

XX /label= Val, Ile, Met, Leu, Phe, Ala, Nle

XX W0200168859-A2.

XX PD 20-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-US08678.  
XX  
XX 16-MAR-2000; 2000US-189816P.  
XX PR 28-NOV-2000; 2000US-0724460.  
XX  
XX (AMGE-) AMGEN INC.  
XX PA  
XX JIng S;  
XX WPI; 2001-611392/70.  
XX  
XX Nucleic acids-encoding interleukin 17 receptor-like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis, and glaucoma  
XX  
XX Claim 21; Page: 158pp; English.  
XX  
XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor-like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, anti-leukemic, renal,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infectivity, and  
XX optically, vascular, cytostatic, anti-leukemic, anti-infectivity and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17R) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infectious (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its components may also be used as diagnostic probes to detect and  
XX quantify the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17R may also be used as  
XX antigens in the production of antibodies against the proteins and in  
XX assays to identify modulators of expression and activity. The  
XX anti-IL17R antibodies and antagonists may also be used to down regulate  
XX expression and activity.  
XX Note: This sequence is not given in the specification but is based on the  
XX human interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
XX and has been created according to information given in claim 21.  
XX  
XX Sequence 738 AA:  
Query Match 97.2%; Score 3720; DB 22; Length 738;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;  
QY 2' DTGCTGKAAAPRCLVANGVCPASNSGLNTFKYDNCNTYLNPFVGNKVIDAONIT 61  
DB 37 DTGCTGWR -----GVCPASNSGLNTFKYDNCNTYLNPFVGNKVIDAONIT 82  
QY 62 ISOTACHOVATVILMSPGALGIEFLKGFVILBELSEGRQCCQLIKDPQLNSFKR 121  
DB 83 ISOTACHOVATVILMSPGALGIEFLKGFVILBELSEGRQCCQLIKDPQLNSFKR 142  
QY 122 TGMESOFFLMMKFETDYFYVVPFSPKRNESNYHFFTRACDILLAPDNLACKPWKP 181  
DB 143 TGMESOFFLMMKFETDYFYVVPFSPKRNESNYHFFTRACDILLAPDNLACKPWKP 202  
QY 182 RNLIWSQSDQVSEFDPHNPFGFFFLYVLYKLKHSQPKRTCKQETTTSCILQN 241  
DB 203 RNLIWSQSDQVSEFDPHNPFGFFFLYVLYKLKHSQPKRTCKQETTTSCILQN 262  
QY 242 VSPGDYIELVDVDTNTRKVMYALKPVESPMASPIRAMAIVPLVWISAFATLFWCR 301

Db 263 VSPGDYIELVDVDTNTRKVMYALKPVESPMASPIRAMAIVPLVWISAFATLFWCR 322  
QY 302 KKOENITSHLDSESSSYTAALPRELPKPKVPLCTSSKQGNEMNVVOCFAFLQ 361  
Db 323 KKOENITSHLDSESSSYTAALPRELPKPKVPLCTSSKQGNEMNVVOCFAFLQ 382  
QY 362 DFCGCEVALDWDVFCICREGQREWIQKIHESQFIIVVCSKGMFYVDKKNKTKHGGGR 421  
Db 383 DFCGCEVALDWDVFCICREGQREWIQKIHESQFIIVVCSKGMFYVDKKNKTKHGGGR 442  
QY 422 GSGKGLFVAVSAIAEKLRQAKQSSAALSFKFIANTFYSCGDPGIDLSKYRLAD 481  
Db 443 GSGKGLFVAVSAIAEKLRQAKQSSAALSFKFIANTFYSCGDPGIDLSKYRLAD 502  
QY 482 NLPQLCSHLHSDRGLEPCQHTROGSRNRTFRSKGSLYVAICNMHQFIDEEPWFEX 541  
Db 503 NLPQLCSHLHSDRGLEPCQHTROGSRNRTFRSKGSLYVAICNMHQFIDEEPWFEX 562  
QY 542 QFVFPFPPPLRYREPVLKFDGLVNDVCMKCPGSDPCLKVEAAVLGATGPADSOHES 601  
Db 563 QFVFPFPPPLRYREPVLKFDGLVNDVCMKCPGSDPCLKVEAAVLGATGPADSOHES 622  
QY 602 OHGGLDQGEARPPALDGSAAQPLHHTVAKGSPDAPRDSGIYDSVPSSELSLPLMEGL 661  
Db 623 OHGGLDQGEARPPALDGSAAQPLHHTVAKGSPDAPRDSGIYDSVPSSELSLPLMEGL 682  
QY 662 STDQTFSTLSTESVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAPV 717  
Db 683 STDQTFSTLSTESVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAPV 738  
RESULT 7  
AAU09951  
ID AAU09951 standard; Protein; 738 AA.  
AC AAU09951;  
XX 14-FEB-2002 (first entry)  
DT Human Interleukin 17 (hIL-17) receptor like protein substitution #1.  
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
XX vascular; cytostatic; anti-leukemic; anti-infectivity; ophthalmological;  
XX vasculitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
XX mutain.  
XX Homo. sapiens.  
XX OS Synthetic.  
XX Key Location/Qualifiers  
XX Misc-difference 45 /label= Gly, Pro or Ala  
XX FT  
XX W0200168859-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-US08678.  
XX  
XX 16-MAR-2000; 2000US-189816P.  
XX PR 28-NOV-2000; 2000US-0724460.  
XX  
XX (AMGE-) AMGEN INC.  
XX PA  
XX JIng S;  
XX WPI; 2001-611392/70.  
XX

PT Nucleic acids encoding interleukin 17 receptor like polypeptides,  
PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
PT diabetes, psoriasis and glaucoma.  
XX  
PS Claim 16; Page -; 158pp; English.  
XX  
CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
CC receptor like polypeptides useful as vaccines and in gene therapy. These  
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infectivity and  
CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
CC proteins may be used to prevent and treat diseases associated with  
CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
CC include, for example immune disorders (e.g. inflammation, diabetes and  
CC transplant rejection), infections (e.g. hepatitis and septicemia),  
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
CC breast cancer), reproductive disorders (e.g. infertility and  
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
CC DNA and its complements may also be used as diagnostic probes to detect and  
CC quantitate the presence of similar nucleic acids in samples and identify  
CC patients needing restorative therapy. The IL17rlp may also be used as  
CC antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of expression and activity. The  
CC anti-IL17rlp antibodies and antagonists may also be used to down regulate  
CC expression and activity.  
CC Note: This sequence is not given in the specification but is based on the  
CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
CC and has been created according to information given in claim 18.  
XX  
SQ Sequence 738 AA;

Query Match 97.14; Score 3718; DB-22; Length 738;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;  
QY 2 DTGCHWKAARPRCLVANGVGPASRNSGLYNTFKYDCTTLNPNVKGVIADAQNI 61  
DB 37 DTGCHW-----GVAPASRNSGLYNTFKYDCTTLNPNVKGVIADAQNI 82  
QY 62 ISQYACHQVAVTILSPGALGTEFLKGFVILELSESGROCOOLILKDPKOLNSFER 121  
DB 83 ISQYACHQVAVTILSPGALGTEFLKGFVILELSESGROCOOLILKDPKOLNSFER 142  
QY 122 TGESOPTLANKFTDITVKKVPFSSIKNESNYHFFTRACDILLOPDMACKPWKP 181  
DB 143 TGESOPTLANKFTDITVKKVPFSSIKNESNYHFFTRACDILLOPDMACKPWKP 202  
QY 182 RNLNISQHSQDMQVSFDRAPHNPGFFFLYHLKHEGPFKRTCKQBTETTSCILQ 241  
DB 203 RNLNISQHSQDMQVSFDRAPHNPGFFFLYHLKHEGPFKRTCKQBTETTSCILQ 262  
QY 242 VSPGDYIIELVDNTRKVMHVALKPVHSPWAGPIRAVAITVPLVWISAFATFTWCR 301  
DB 263 VSPGDYIIELVDNTRKVMHVALKPVHSPWAGPIRAVAITVPLVWISAFATFTWCR 322  
QY 302 KKOENITSHLDESSSYTAAIPRELPRKVPCLCTSSKDGONHNVVQCFATFLO 361  
DB 323 KKOENITSHLDESSSYTAAIPRELPRKVPCLCTSSKDGONHNVVQCFATFLO 382  
QY 362 DFCGCVALDWDPSLCRSGREWIYQIKHESOFITVCSKGMKYFVKKYHKGGR 421  
DB 383 DFCGCVALDWDPSLCRSGREWIYQIKHESOFITVCSKGMKYFVKKYHKGGR 442  
QY 422 GSGKGLFVAVSAIAKLRQAKQSSAALSFAITVFDYSCGDVPGILDLSKYRLMD 481  
DB 443 GSGKGLFVAVSAIAKLRQAKQSSAALSFAITVFDYSCGDVPGILDLSKYRLMD 502

QY 482 NLPOLCSHLHSRDEGLQEQCOHTROGSRNATPFSKSGSLKVAICMHOFTDEPDWPK 541  
DB 503 NLPOLCSHLHSRDEGLQEQCOHTROGSRNATPFSKSGSLKVAICMHOFTDEPDWPK 562  
QY 542 QVFPFPPPLRYREPLEKFDGLVNDVWCKPDSDFCLKVAALVATGATGADSOHES 601  
DB 563 QVFPFPPPLRYREPLEKFDGLVNDVWCKPDSDFCLKVAALVATGATGADSOHES 622  
QY 602 QHGGLDQCEARPALDQSAALQLEFVTKAGSPDPRSDGYDSSVPSSELSPLAKGL 661  
DB 623 QHGGLDQCEARPALDQSAALQLEFVTKAGSPDPRSDGYDSSVPSSELSPLAKGL 682  
QY 662 STDQFETSLTESVSSSGIGEEPPALPSPKLLSSGSKADLCGRSTYDELEAVAP 717  
DB 683 STDQFETSLTESVSSSGIGEEPPALPSPKLLSSGSKADLCGRSTYDELEAVAP 738  
RESULT 8  
AAU09952  
ID AAU09952 standard; Protein; 738 AA.  
XX  
AC AAU09952;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #2.  
XX  
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
KW vascular; cytostatic; anti-leukaemic; anti-infectivity; ophthalmological;  
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
KW muteln.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 227 /label= Phe, Leu, Val, Ile, Ala, Tyr  
XX  
PN WC200168859-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 15-MAR-2001; 2001WO-0508678.  
XX  
PR 16-MAR-2000; 2000US-189816P.  
PR 28-NOV-2000; 2000US-0724460.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Jing S;  
XX  
PI WPI; 2001-611392/70.  
XX  
DR Nucleic acids encoding interleukin 17 receptor like polypeptides,  
PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
PT diabetes, psoriasis and glaucoma.  
XX  
PS Claim 19; Page -; 158pp; English.  
XX  
CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
CC receptor like polypeptides useful as vaccines and in gene therapy. These  
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infectivity and  
CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
CC proteins may be used to prevent and treat diseases associated with

CC inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection); infections (e.g. hepatitis and septicemia);  
 CC weight disorders (e.g. anorexia, cachexia and obesity); neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy);  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema); skin disease  
 CC (e.g. eczema and psoriasis); kidney disease (e.g. glomerulonephritis);  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia); vascular disorders  
 CC (e.g. stroke and atherosclerosis); cancers (e.g. leukemia, myeloma and  
 CC breast cancer); reproductive disorders (e.g. infertility and  
 CC miscarriage); eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantify the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rip may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rip antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)  
 CC and has been created according to information given in claim 19.  
 CC  
 XX Sequence: 738 AA;

Query Match 97.1%; Score 3718; DB 22; Length 738;  
 Best Local Similarity 97.6%; Pred. No. 0;  
 Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;  
 2 DTCGRMKAARPLCVANEGVGRASRNSGLNTPKYNCTYTLNPGVGHVADQAQNT 61  
 37 DTCGRMKAARPLCVANEGVGRASRNSGLNTPKYNCTYTLNPGVGHVADQAQNT 82  
 62 ISOYACHQDVANTILSPGALGIEFKGRVILEELKSGRCQOLILKDPKOLNSPFR 121  
 83 ISOYACHQDVANTILSPGALGIEFKGRVILEELKSGRCQOLILKDPKOLNSPFR 142  
 122 TGHSOPFLANKFETDFVKVYVFPFISANESNTHPFFETACDILLQDNLACKPFWKP 181  
 143 TGHSOPFLANKFETDFVKVYVFPFISANESNTHPFFETACDILLQDNLACKPFWKP 202  
 182 RNLNLSQSGDMQVSDPHAFNFGFRFFLYHKLKHEGPKFKTKCKOBTETTSCLLN 241  
 203 RNLNLSQSGDMQVSDPHAFNFGFRFFLYHKLKHEGPKFKTKCKOBTETTSCLLN 262  
 242 VSPGDIYIELVDNTNTRKVNIAKLVHSPWAGPIRAVAITVPLVISAFAFLPFWCR 301  
 263 VSPGDIYIELVDNTNTRKVNIAKLVHSPWAGPIRAVAITVPLVISAFAFLPFWCR 322  
 302 KQOENIYSHLDESSESTITAAIPRLRPRKRVFLCYSSKQGNMNVVQCFAYFLQ 361  
 323 KQOENIYSHLDESSESTITAAIPRLRPRKRVFLCYSSKQGNMNVVQCFAYFLQ 382  
 362 DFCGCEVALDWEFSLCREGORENVIOKIHESOFIIVVCSGKMKYFVDKNTKHKGGGR 421  
 383 DFCGCEVALDWEFSLCREGORENVIOKIHESOFIIVVCSGKMKYFVDKNTKHKGGGR 442  
 422 GSGKGLFLVAVSAIAELKRAQSSAALSKFIATVDTYSCGDVPGIILDSTKYLMD 481  
 443 GSGKGLFLVAVSAIAELKRAQSSAALSKFIATVDTYSCGDVPGIILDSTKYLMD 502  
 482 NLPQLCSHLSDRHGLQEPQQTQGGRRNTPFKSGRSLYVATCNKHQIDEEPWFKEK 541  
 503 NLPQLCSHLSDRHGLQEPQQTQGGRRNTPFKSGRSLYVATCNKHQIDEEPWFKEK 562  
 542 QVPVPHPPPLRYREPVLEKFGSLVLDVNMCKPGPSDFCLKVAEAVLGATGPADSOHES 601  
 563 QVPVPHPPPLRYREPVLEKFGSLVLDVNMCKPGPSDFCLKVAEAVLGATGPADSOHES 622  
 602 QRGGLDQGEARALDGSAAQLPLHIVKAGSPDMPRDSIGTDSVPSSLSLIMGL 661  
 623 QRGGLDQGEARALDGSAAQLPLHIVKAGSPDMPRDSIGTDSVPSSLSLIMGL 682  
 662 STDQTESLITSSVSSSGLGEEPPALPSKLLSSGSCNCKADLCGRSTYDELHNAV 717

Db 683 STDQTESLITSSVSSSGLGEEPPALPSKLLSSGSCNCKADLCGRSTYDELHNAV 738

# RESULT 9

AA009956  
 ID AA009956 standard; Protein; 738 AA.

XX AA009956

AC AA009956

XX 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutant.

XX Homo sapiens

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 515

FT /label= Asp, Glu

XX WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX (ANGE-) ANGEN INC.

XX Jing S;

XX WPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,  
 diabetes, psoriasis and glaucoma.

XX Claim 23; Page -: 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 receptor like polypeptides useful as vaccines and in gene therapy. These  
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, renal,  
 osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and  
 ophthalmological activities. The IL-17 receptor like nucleic acids and  
 proteins may be used to prevent and treat diseases associated with  
 inappropriate IL-17 receptor like polypeptide (IL17rip) expression. These  
 include, for example immune disorders (e.g. inflammation, diabetes and  
 transplant rejection), infections (e.g. hepatitis and septicemia),  
 weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 breast cancer), reproductive disorders (e.g. infertility and  
 miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 DNA and its complements may also be used as diagnostic probes to detect and  
 quantify the presence of similar nucleic acids in samples and identify  
 patients needing restorative therapy. The IL17rip may also be used as



CC antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of expression and activity. The  
CC anti-IL17R1p antibodies and antagonists may also be used to down regulate  
CC expression and activity.  
CC Note: This sequence is not given in the specification but is based on the  
CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
CC and has been created according to information given in claim 23.  
XX  
SQ Sequence 738 AA;

Query Match 97.1%; Score 3718; DB 22; Length 738;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

QY 2 DTCCGRKAAARPLCVAEGVGPASRNSCLNITFKYDCTTYLNPVGRKVIADAQNI 61  
DB 37 DTCCGR-----GVGPASRNSCLNITFKYDCTTYLNPVGRKVIADAQNI 82  
QY 62 ISQACHDQAVTILWSPGALGIEFLAGFRVILELSEGRCCOOLILDPKOLNSSFR 121  
DB 83 ISQACHDQAVTILWSPGALGIEFLAGFRVILELSEGRCCOOLILDPKOLNSSFR 142  
QY 122 TMSQSPFLANKETDYFVKKVPPSPKESNTHPPFTRACDILLOPDNKLACFPK 181  
DB 143 TMSQSPFLANKETDYFVKKVPPSPKESNTHPPFTRACDILLOPDNKLACFPK 202  
QY 182 RNLNISQSGDMQVSDHAPNPGCFRFFLYHLKLBHEGPFRRKTCBOQTETTSCL 241  
DB 203 RNLNISQSGDMQVSDHAPNPGCFRFFLYHLKLBHEGPFRRKTCBOQTETTSCL 262  
QY 242 YSPGDIYIELVDNTIRKVAHYALKFVSPWAGTRAVITVPLVVISAFATLTVM 301  
DB 263 YSPGDIYIELVDNTIRKVAHYALKFVSPWAGTRAVITVPLVVISAFATLTVM 322  
QY 302 KQOENIYSHLDESSESTYTAALPRELRPRPKVELCYSSKDGQNNHNVQCFAT 361  
DB 323 KQOENIYSHLDESSESTYTAALPRELRPRPKVELCYSSKDGQNNHNVQCFAT 382  
QY 362 DPCCCEVALDWEFLSREGORWVLOKHESQPIIVVCSKGMKYPDKNKKGGGR 421  
DB 383 DPCCCEVALDWEFLSREGORWVLOKHESQPIIVVCSKGMKYPDKNKKGGGR 442  
QY 422 SSGGELFLVAVSAIAEKLRQAKQSSAALSKFIAYVDYSCGDVPGILDLSIR 481  
DB 443 SSGGELFLVAVSAIAEKLRQAKQSSAALSKFIAYVDYSCGDVPGILDLSIR 502  
QY 482 NLPOLCSHLSRHDGLQEPGORTGSGRRNFRSKSGSLVAICNNHOFIDEEP 541  
DB 503 NLPOLCSHLSRHDGLQEPGORTGSGRRNFRSKSGSLVAICNNHOFIDEEP 562  
QY 542 QPVPFPPLPYRREPVLKFDGLVNDVCKPGEPSDFCLKVEAAVLGATGPDSQ 601  
DB 563 QPVPFPPLPYRREPVLKFDGLVNDVCKPGEPSDFCLKVEAAVLGATGPDSQ 622  
QY 602 QHGLDQDGEARPLDGSANQPLHLYVAGSPDMPSDGIYDSSVPSSELSPL 661  
DB 623 QHGLDQDGEARPLDGSANQPLHLYVAGSPDMPSDGIYDSSVPSSELSPL 682  
QY 662 STDTTSTSTESVSSSGIAGEEPPLPFLSKLSSGCKADLCGRSTYDELH 717  
DB 683 STDTTSTSTESVSSSGIAGEEPPLPFLSKLSSGCKADLCGRSTYDELH 738

RESULT 10  
AAU09955  
ID AAU09955 standard; Protein: 738 AA.  
XX  
AC AAU09955;  
XX

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.

XX

KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
KW hepatic; anabolic; anorectic; anti-Alzheimer's; anti-parkinsonian;  
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
mutel.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 385  
FT /Label- Cys, Ser, Ala  
XX  
XX WO200168859-A2  
XX  
XX 20-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-US08678.  
XX  
XX 16-MAR-2000; 2000US-189816P.  
XX 28-NOV-2000; 2000US-074460.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Jing S;  
XX  
XX WPI; 2001-611392/70..

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma.  
XX  
XX Claim 22; Page 1; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-Alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17R1p) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic-fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantitate the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17R1p may also be used as  
XX antigens in the production of antibodies against the proteins and in  
XX assays to identify modulators of expression and activity. The  
XX anti-IL17R1p antibodies and antagonists may also be used to down regulate  
XX expression and activity.

XX Note: This sequence is not given in the specification but is based on the  
XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
XX and has been created according to information given in claim 22.

XX Sequence 738 AA;

Query Match 97.0%; Score 3714; DB 22; Length 738;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;





Db 203 RNILNSQSDMQVSDHAPNFGFPEYLLKLEHGPFFKRCQBOZTETTSCILQN 262  
 QY 242 VSRGDIYIELVDYNTNTRKWHYALKVPSWAGIRAVATVPLVWISAPFLTVNCR 301  
 Db 263 VSRGDIYIELVDYNTNTRKWHYALKVPSWAGIRAVATVPLVWISAPFLTVNCR 322  
 QY 302 KQOENIYSHLDESESTTAAALPRERLRPRKPVFLCYSSKQGNHNNVOCPAYFLQ 361  
 Db 323 KQOENIYSHLDESESTTAAALPRERLRPRKPVFLCYSSKQGNHNNVOCPAYFLQ 382  
 QY 362 DFCGCEVALDWFSLCREGQREWYIQKHESQFIIVVCSKGMKTFYDKNKYKKGGR 421  
 Db 383 DFCGCEVALDWFSLCREGQREWYIQKHESQFIIVVCSKGMKTFYDKNKYKKGGR 442  
 QY 422 GSGGELFLVNSAALKRQKSSAALSFKFIAYVIFDSCGDVPGILDSTYRLMD 481  
 Db 443 GSGGELFLVNSAALKRQKSSAALSFKFIAYVIFDSCGDVPGILDSTYRLMD 502  
 QY 482 NLPOCLSHLSRDBGLQEPGQHTQSGSRNYPRSKGSLVVALCNHGFIDEEPWFEX 541  
 Db 503 NLPOCLSHLSRDBGLQEPGQHTQSGSRNYPRSKGSLVVALCNHGFIDEEPWFEX 562  
 QY 542 QVFPFPPPLRNPVLEKFDGSLVLDVNCVCPGSPESDFCLKVEAVLGATGPADSOHES 601  
 Db 563 QVFPFPPPLRNPVLEKFDGSLVLDVNCVCPGSPESDFCLKVEAVLGATGPADSOHES 622  
 QY 602 QRGGLDGDGSPALDGAALQPLLEHTVYKAGSPDNRDSCIYDSSVSPSELSPMBGL 661  
 Db 623 QRGGLDGDGSPALDGAALQPLLEHTVYKAGSPDNRDSCIYDSSVSPSELSPMBGL 682  
 QY 662 STDQTTSSITSSVSSGIEEPALPSPKLLSSGCKADLCGRSTYDELHAPV 717  
 Db 683 STDQTTSSITSSVSSGIEEPALPSPKLLSSGCKADLCGRSTYDELHAPV 738

RESULT 12  
 ID AN004958 standard; Protein: 728 AA.  
 AC AN004958;  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE Human Interleukin 17 receptor, IL-17RH4.  
 KW Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;  
 KW PRO20026; DNA 154095-2998; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 OS Homo sapiens.  
 FH Key  
 FT Region  
 FT Location/Qualifiers  
 FT 19..24 "N-myristoylation site"  
 FT 31..34 "N-myristoylation site"  
 FT Modified-site  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site  
 FT 38..41 "N-myristoylation site"  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site  
 FT 56..59 "N-myristoylation site"  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site  
 FT 113..116 "N-myristoylation site"  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site  
 FT 147..150 "N-myristoylation site"  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site  
 FT 182..185 "N-myristoylation site"  
 FT /note="Asn is N-glycosylated"  
 FT Modified-site  
 FT 232..235 "N-myristoylation site"  
 FT /note="Asn is N-glycosylated"  
 FT Region  
 FT /note="cAMP/GMP-dependent protein kinase  
 FT phosphorylation site"  
 FT 266..269  
 FT Modified-site  
 FT /note="Asn is N-glycosylated"

FT Domain  
 FT 283..307 /note="Transmembrane domain"  
 FT Region  
 FT 312..319 /note="Tyrosine kinase phosphorylation site"  
 FT Region  
 FT 375..380 /note="N-myristoylation site"  
 FT Region  
 FT 416..424 /note="Tyrosine kinase phosphorylation site"  
 FT Region  
 FT 428..433 /note="N-myristoylation site"  
 FT Region  
 FT 429..434 /note="N-myristoylation site"  
 FT Region  
 FT 432..437 /note="N-myristoylation site"  
 FT Region  
 FT 433..436 /note="Glycosaminoglycan attachment site"  
 FT 517..522 /note="N-myristoylation site"  
 FT Region  
 FT 574..579 /note="N-myristoylation site"  
 FT Region  
 FT 652..657 /note="N-myristoylation site"  
 FT Region  
 FT 707..712 /note="N-myristoylation site"  
 FT Region  
 FT 707..712 /note="N-myristoylation site"  
 XX  
 PN W0200146420-A2.  
 XX  
 XX 28-JUN-2001.  
 XX  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX  
 XX 23-DEC-1999; 99US-0172096.  
 XX 30-DEC-1999; 99WO-US31274.  
 XX 11-JAN-2000; 2000US-0175481.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 21-MAR-2000; 2000US-0191007.  
 XX 02-JUN-2000; 2000WO-US07532.  
 XX 22-JUN-2000; 2000WO-US15264.  
 XX 22-AUG-2000; 2000US-0213087.  
 XX 24-AUG-2000; 2000WO-064848.  
 XX 24-OCT-2000; 2000US-0242837.  
 XX 28-NOV-2000; 2000WO-US30873.  
 XX 01-DEC-2000; 2000US-0253646.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX (GETH) GENENTECH INC.  
 XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ,  
 XX Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;  
 XX Watanabe CK, Williams PM, Wood WI, Yansura DG;  
 XX WPI; 2001-451708/48.  
 XX N-PSDB; AAS09517.  
 XX  
 XX Novel PRO polypeptides homologous to interleukin-17, useful for the  
 XX diagnosis and treatment of immune related disease e.g. rheumatoid  
 XX arthritis and diabetes.  
 XX  
 XX Claim 10; Fig 18; 188pp; English.  
 XX  
 XX The sequence is PRO20026 which is the human Interleukin 17 receptor,  
 XX IL-17RH4, encoded by DNA 154095-2998. A composition  
 XX containing ant/agonists to the PRO polypeptides or individual components  
 XX are useful for treating a mammal with an immune related disease, e.g.  
 XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 XX disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 XX disease, contact dermatitis, an allergic disease e.g. food



Db 42 QGVGPASRNSGLNITFYDKNTYLNPKVGHVIADAOQNTISQYACHQVAVTILMSFG 101  
 QY 81 ALGIEFLKGRVITLDELSEKROOQILILKDKQLNLSFKTKTGHESOPFLANKFTDYFV 140  
 Db 102 ALGIEFLKGRVITLDELSEKROOQILILKDKQLNLSFKTKTGHESOPFLANKFTDYFV 161  
 QY 141 KVPFPPSIKSHSNHPPFRFRACDILLOPDLNACKPFWKPRNLTISQSGDMQVSFOHA 200  
 Db 162 KVPFPPSIKSHSNHPPFRFRACDILLOPDLNACKPFWKPRNLTISQSGDMQVSFOHA 221  
 QY 201 PHNGGFFFTLYLKLHSGPPFRKTKQOYTTTSCLLQNSGDIYIELVDDNTYTRK 260  
 Db 222 PHNGGFFFTLYLKLHSGPPFRKTKQOYTTTSCLLQNSGDIYIELVDDNTYTRK 281  
 QY 261 VGHYALPVSHPWAGPIRAVAITVPLVWISAFATLFTVCKKQENITSHLDESSSS 320  
 Db 282 VGHYALPVSHPWAGPIRAVAITVPLVWISAFATLFTVCKKQENITSHLDESSSS 341  
 QY 321 TTTAALPRELRPRKPVLYTSSKDGQNNMNVVQCFATLQDCGCEVALDWEFSLCR 380  
 Db 342 TTTAALPRELRPRKPVLYTSSKDGQNNMNVVQCFATLQDCGCEVALDWEFSLCR 401  
 QY 381 EQRENWYQIHESQFIIVVCSKGMKTFVOKNYKHGGGSGKGLFLVAVSAIAEKL 440  
 Db 402 EQRENWYQIHESQFIIVVCSKGMKTFVOKNYKHGGGSGKGLFLVAVSAIAEKL 461  
 QY 441 ROAKQSSAALSFAVTFDSCBQVPGILDLSTKYRLMDNLPQLCSHLHSDRGLQEP 500  
 Db 462 ROAKQSSAALSFAVTFDSCBQVPGILDLSTKYRLMDNLPQLCSHLHSDRGLQEP 521  
 QY 501 GQHTROGSRNTFRSKSGSLYVAICNMHOFIDEEPWFQFVPPHPPPLATREPVLEK 560  
 Db 522 GQHTROGSRNTFRSKSGSLYVAICNMHOFIDEEPWFQFVPPHPPPLATREPVLEK 581  
 QY 561 FDSGLVLDNVMCKRPESDFCLKVEAVLGNTPADSOHSGHGLDQDGEARPALDGA 620  
 Db 582 FDSGLVLDNVMCKRPESDFCLKVEAVLGNTPADSOHSGHGLDQDGEARPALDGA 641  
 QY 621 ALQPLLTIVKAGSPMDRSGIYDSVPSSLSPLMEGLSTDTQTSLSLTVSSSSG 680  
 Db 642 ALQPLLTIVKAGSPMDRSGIYDSVPSSLSPLMEGLSTDTQTSLSLTVSSSSG 701  
 QY 681 LGREEPPALPSKLLSGGSKADLGRSYTDELHVAVPL 718  
 Db 702 LGREEPPALPSKLLSGGSKADLGRSYTDELHVAVPL 739

## RESULT 14

AAU11355  
 ID AAU11355 standard; Protein: 738 AA.

AC AAU11355;

XX 26-MAR-2002 (first entry)

XX Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.

DE Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;  
 KW gene therapy; protein therapy; immunological disorder.

XX Homo sapiens.

XX Key: Location/Qualifiers

FT Misc-difference 25 /label= Val

FT /note= "Encoded by GTN"

XX WO200190358-A2.

XX 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US16767.

PR 24-MAY-2000; 2000US-206862P.  
 XX (SCHE ) SCHERING CORP.  
 PA Gorman DM;  
 XX WPI; 2002-106198/14.  
 DR N-FSD8; AAS18134.  
 XX Isolated antigenic human or mouse DNAX receptor subunit-like  
 PT polypeptide useful for detecting antibodies generated in response to  
 PT presence of increased protein levels or immunological disorders -  
 XX Claim 1; Page 25; 148pp; English.

XX The invention relates to primate and rodent DNAX cytokine receptor  
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The  
 CC receptors, or their portions may be useful as phosphate labelling enzymes  
 CC to label general or specific substrates. The subunits may also be  
 CC capable of binding antibodies. A combination, e.g., including a DCRS can  
 CC be used as an immunogen for the production of antisera or antibodies  
 CC capable of distinguishing between other cytokine receptor family members.  
 CC A purified DCRS can also be used as a reagent to detect antibodies  
 CC generated in response to the presence of elevated levels of expression,  
 CC or immunological disorders which lead to antibody production to the  
 CC endogenous receptor. This sequence represents the human DCRS8  
 CC polypeptide.

XX Sequence 738 AA;

Query Match 95.58; Score 3657.5; DB 23; Length 738;

Best Local Similarity 96.48; Pred. No. 0;

Matches 692; Conservative 2; Mismatches 9; Indels 15; Gaps 2;

QY 1 ADTCGRWKAARAPRLCVNMGVGPASRNSGLNITFYDKNTYLNPKVGHVIADAOQNI 60  
 Db 36 ADTCW-----XGVGPASRNSGLNITFYDKNTYLNPKVGHVIADAOQNI 81  
 QY 61 TISQYACHQVAVTILMSFGALGIEFLKGRVILEELKSGROCOQLILKDKQLNLSFK 120  
 Db 82 TISQYACHQVAVTILMSFGALGIEFLKGRVILEELKSGROCOQLILKDKQLNLSFK 141  
 QY 121 RTGMSQPLANKFETDYFVKVPPFPIKSNYTHPPFFTRACDILLOPDLNACKPFWK 180  
 Db 142 RTGMSQPLANKFETDYFVR-LSPFPIKSNYTHPPFFTRACDILLOPDLNACKPFWK 200  
 QY 181 PRNLTISQSGDMQVSFOHAPHNGFRFFTLVHLKHEGPKTKCKQOYTTTSCLLQ 240  
 Db 201 PRNLTISQSGDMQVSFOHAPHNGFRFFTLVHLKHEGPKTKCKQOYTTTSCLLQ 260  
 QY 241 NVSPGDTIELVDDNTYTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVNC 300  
 Db 261 NVSPGDTIELVDDNTYTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVNC 320  
 QY 301 RKQENITSHLDESSSSTYTAALPRELRPRKPVLYTSSKDGQNNMNVVQCFATFL 360  
 Db 321 RKQENITSHLDESSSSTYTAALPRELRPRKPVLYTSSKDGQNNMNVVQCFATFL 380  
 QY 361 QDCGCEVALDWEFSLCRREGQEWYQKHESQFIIVVCSKGMKTFVOKNYKHGGG 420  
 Db 381 QDCGCEVALDWEFSLCRREGQEWYQKHESQFIIVVCSKGMKTFVOKNYKHGGG 440  
 QY 421 RGSKGELFLVAVSAIAEKLROAKQSSAALSFAVTFDSCBQVPGILDLSTKYRLM 480  
 Db 441 RGSKGELFLVAVSAIAEKLROAKQSSAALSFAVTFDSCBQVPGILDLSTKYRLM 500  
 QY 481 DNLPLQCSHLHSDRGLQEPQOHTROGSRNTFRSKSGSLYVAICNMHOFIDEEPWF 540  
 Db 501 DNLPLQCSHLHSDRGLQEPQOHTROGSRNTFRSKSGSLYVAICNMHOFIDEEPWF 560  
 QY 541 KQVFPHPPLATREPVLEKFDGLVLDNVMCKRPESDFCLKVEAVLGNTPADSOH 600

Db 561 KQVPPHPPPLTREPVLKFDGLVNDVAKCPGSPDCLKVEAAVLGATGPAQSQHE 620  
QY 601 SQGGGLDQGEARALDGSAAQLPILHTVAGSPSDMPDGGTIDSSVPSSELSLPLMBG 660  
Db 621 SQGGGLDQGEARALDGSAAQLPILHTVAGSPSDMPDGGTIDSSVPSSELSLPLMBG 680  
QY 661 LSTDOETSSLTSSVSSSSGLGEEPPALPKSLSSGCKADLCGRSTDEHAYAPL 718  
Db 681 LSTDOETSSLTSSVSSSSGLGEEPPALPKSLSSGCKADLCGRSTDEHAYAPL 738

RESULT 15

AB07630  
ID: AB07630, standard; Protein; 739 AA.  
AC AB07630;  
XX  
XX 20-MAY-2002 (first entry)  
DE Murine cytokine receptor, zcytor18.  
DE Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;  
DE pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
DE erythroleukemia; chromosome 3p14.3; gene therapy; mouse.  
OS Mus sp.  
XX  
XX W0200208259-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 23-JUL-2001; 2001MO-US23253.  
XX  
XX 26-JUL-2000; 2000US-220747P.  
XX  
XX (ZIMO) ZYMOGENETICS INC.  
XX  
XX Presnell SR, Kuestner RE, Gao Z;  
XX  
XX WPI; 2002-217048/27.  
XX  
XX N-PSDB; ABA95037, ABA95038.  
XX  
XX New cytokine receptor polypeptide designated zcytor18, useful for  
XX inhibiting cell proliferation associated with psoriasis or tumor  
XX growth, and modulating immune system by binding to endogenous zcytor18  
XX ligand

Claim 1: Page 111-115; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide designated zcytor18. The zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumor growth. The encoding nucleic acids are useful for providing zcytor18 in vivo by gene therapy techniques. zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the zcytor18 probes and primers can be used to detect and localize zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosomes 3 in which zcytor18 gene resides. The zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial periodic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a murine zcytor18 amino acid sequence.

Sequence 739 AA;  
Query Match 83.8%; Score 3208; DB 23; Length 739;  
Best Local Similarity 84.6%; Pred. No. 1.3e-308;  
Matches 611; Conservative 37; Mismatches 52; Indels 22; Gaps 6;  
QY 1 ADTCGWRKKAARPLCVANEGVGPASRNSGLNITFKYDNCCTVYLNQ-VCKHVIADAQN 59  
Db 36 ADTCGHR-----GVGPASRNSGLNITFRDNCCTVYLNQ-VCKHVIADAQN 81

QY 60 ITISYACHDOAVTILNPGALGIEFLKGFVILIELSEKSGCCOQILKDPQLNSSF 119  
Db 82 ITISYACHDOAVTILNPGALGIEFLKGFVILIELSEKSGCCOQILKDPQLNSSF 141  
QY 120 KTGHSOFTPLAKFFETDFTVAVPPPSIKNESNYHPPFFTRACDILLOPDHACKPFW 179  
Db 142 KTGHSOFTPLAKFFETDFTVAVPPPSIKNESNYHPPFFTRACDILLOPDHACKPFW 201  
QY 180 KPRNLNISOHSDNOVSFDHAPNFGFFFYHLKLGHEGPKKTKCQKQETTTSCLL 239  
Db 202 KPRNLNISOHSDNOVSFDHAPNFGFFFYHLKLGHEGPKKTKCQKQETTTSCLL 261  
QY 240 QNVSPGDIYIELVDDTNTTKVNYHTALFVSPWAGPIRAVAITVPLVVISAFATLFTVM 299  
Db 262 QNVSPGDIYIELVDDTNTTKVNYHTALFVSPWAGPIRAVAITVPLVVISAFATLFTVM 321  
QY 300 CRKQENIYSHLDESESSSTYTAALPRERLRPRKPVFLCYSSKQGNMNVVQCFAFY 359  
Db 322 CRKQENIYSHLDESESSSTYTAALPRERLRPRKPVFLCYSSKQGNMNVVQCFAFY 381  
QY 360 LQDFGCEVALDLWEDFSLCREQENYIOKIHESOFILVCSGKMYPVOKNTHKGG 419  
Db 382 LQDFGCEVALDLWEDFSLCREQENYIOKIHESOFILVCSGKMYPVOKNTHKGG 441  
QY 420 GRGSGEGELFVAVSAIAELKQAKQSSAALSKFTAVTFTSCBDVPGILDSTKYL 479  
Db 442 SRGAQGEFFLVAVAAIAELKQAKQSSAALSKFTAVTFTSCBDVPGILDSTKYL 501  
QY 480 MONTPLQCSHLHSHRDEGLQEP-GOHTRQSGRRNYFRSKSGSLTYAICNMHOFIDEEPW 538  
Db 502 MDLPELCAHLES---GEQEVLGQHPGHSSRRNYFRSKSGSLTYAICNMHOFIDEEPW 558  
QY 539 FEKQVPPHPPPLTREPVLKFDGLVNDVAKCPGSPDCLKVEAAVLGATGPAQSQ 598  
Db 559 FEKQVPPHPPPLTREPVLKFDGLVNDVAKCPGSPDCLKVEAAVLGATGPAQSQ 618  
QY 599 H--ESQHGGLDQGEARALDGSAAQLPILHTVAGSPSDMPDGGTIDSSVPSSELSL 656  
Db 619 STLESQHVGLDQGEARALDGSAAQLPILHTVAGSPSDMPDGGTIDSSVPSSELSL 678  
QY 657 LMEGSLSTQHTSTSLTSTSSSSGLGEEPPALPKSLSSGCKADLCGRSTDEHAYAPL 716  
Db 679 LMEGSLSTQHTSTSLTSTSSSSGLGEEPPALPKSLSSGCKADLCGRSTDEHAYAPL 737  
QY 717 PL 718  
Db 738 PL 739

Search completed: May 19, 2003, 09:20:01  
Job time : 58.0074 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:16:08 ; Search time 26.5067 Seconds

(without alignments)  
(604.041 Million cell updates/sec)

Title: US-09-912-157-2\_copy\_36\_753

Perfect score: 3829  
Sequence: 1 ADTCGRMKAAAPRLCVAN.....CFADLGRSTYDELHVAFL 718

Scoring table: BLOSUM62

Gapop 10.0 ; Gapart 0.5

Searched: 283224 seqs, 95134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR73:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3005	78.5	564	2 T42695	hypothetical prote
2	170.5	4.5	846	2 T27282	hypothetical prote
3	126.5	3.3	718	2 T30113	hypothetical prote
4	117	3.1	757	2 T09081	telomere-associate
5	116.5	3.0	901	2 F83781	transposase (88) /
6	110	2.9	535	2 T17212	hypothetical prote
7	110	2.9	592	2 T49239	vesicle transport
8	110	2.9	917	2 T04661	hypothetical prote
9	109	2.8	998	2 S37627	protein-tyrosine k
10	107.5	2.8	938	2 T49071	protein kinase - m
11	107.5	2.8	3788	2 T13960	beige protein homo
12	107.5	2.8	3942	2 T42730	Bassoon protein -
13	106.5	2.8	638	2 D86477	lysosomal traffic
14	106	2.8	3788	2 T30851	dead ringer nuclea
15	105	2.7	901	2 JC6093	zinc finger protei
16	105	2.7	1571	2 T14155	protein-tyrosine-p
17	104	2.7	1462	1 B36182	GTPase-activating
18	103.5	2.7	663	2 A39897	Argonaute (AGO1)-1
19	103.5	2.7	930	2 A84668	ABR protein 2 - hu
20	102	2.7	813	2 B47485	98K GTPase-activ
21	102	2.7	859	2 A49307	Subtilase family p
22	102	2.7	1448	2 A12007	ABR protein 1 - hu
23	101.5	2.7	822	2 A47485	probable sensory t
24	101.5	2.7	1639	2 T50119	hypothetical prote
25	101	2.6	641	2 T05497	ARR2 protein [mpo
26	101	2.6	664	2 T51247	nucleotide exchang
27	101	2.6	1275	2 A38985	hypothetical prote
28	100.5	2.6	1007	2 T24643	serine/threonine p
29	99.5	2.6	657	2 E96949	

30 99.5 2.6 794 2 S59069  
31 99.5 2.6 981 1 F0WVGM  
32 99 2.6 341 2 H71716  
33 99 2.6 783 2 A31491  
34 99 2.6 970 2 S63039  
35 98.5 2.6 353 2 T33782  
36 98.5 2.6 963 2 AD3881  
37 98.5 2.6 1050 2 G86582  
38 98.5 2.6 1050 2 H72041  
39 98.5 2.6 1050 2 C81624  
40 98 2.6 820 2 S33794  
41 98 2.6 1023 2 T48997  
42 97.5 2.5 291 2 F86451  
43 97.5 2.5 589 2 F96599  
44 97.5 2.5 1121 2 T25715  
45 97 2.5 984 2 A39753

## ALIGNMENTS

### RESULT 1

T42695

hypothetical protein DRFZp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

C:Accession: T42695

R:Blöcker, H.; Boeher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: 222230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DRFZp434N1928

C:Genetics:

A:Note: DRFZp434N1928.1

Query Match 78.5%; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8%; Pred. No. 4.7e-231;

Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 HPFFETRACDILLQPDNLACKPFWKPRNLINISQSGSDMVQSFDPHAFNFGFPFYLHYK 214  
DB 1 HPFFETRACDILLQPDNLACKPFWKPRNLINISQSGSDMVQSFDPHAFNFGFPFYLHYK 60  
QY 215 LKHGPEKRECKQOTTETSCLLQNVSPGDYILLEVDNTTRKVMYALKPVHSPWA 274  
DB 61 LKHGPEKRECKQOTTETSCLLQNVSPGDYILLEVDNTTRKVMYALKPVHSPWA 120  
QY 275 GPIRAVAITVPLVVISAPATLFTVCKRKQENIYSHLDESSESSTYTAALPRELRPR 334  
DB 121 GPIRAVAITVPLVVISATLFTVCKRKQENIYSHLDESSESSTYTAALPRELRPR 180  
QY 335 PRVFLCYSSKDGQNNVVOCCFATFLQDFCGCEVALDWEDEFSLCRGQRENVIOKIHES 394  
DB 181 PRVFLCYSSKDGQNNVVOCCFATFLQDFCGCEVALDWEDEFSLCRGQRENVIOKIHES 240  
QY 395 OFIIVVCSKGMKYFVDKKNYKHGGRSGCKGELFLVAVSAIAEKLRQAKQSSAALSFK 454  
DB 241 OFIIVVCSKGMKYFVDKKNYKHGGRSGCKGELFLVAVSAIAEKLRQAKQSSAALSFK 300  
QY 455 IATVDFSCBEDVPGLDLSKTYRLMDNLPQLCSHLHSRDGLQEQPQHTROGSRNFR 514  
DB 301 IATVDFSCBEDVPGLDLSKTYRLMDNLPQLCSHLHSRDGLQEQPQHTROGSRNFR 360  
QY 515 SKSGRSLYAICNMHQFIDEEPWFKEQFVPPFPPLRYREPFLYLEKFDGSLVNDVNCKP 574  
DB 361 SKSGRSLYAICNMHQFIDEEPWFKEQFVPPFPPLRYREPFLYLEKFDGSLVNDVNCKP 420  
QY 575 GPESDFCLVYEAVALGATGPADSOHSGHGLDQGEARPALDGSAAALPPLHTYAGSP 634

Db 431 GPESDFCLVAAVLGATGPADESQESQSGGLDQGEARPALDGSAAQLPILHFKVAGSP 480  
 QY 635 SDMPRSGIYDSSVPSSELSPLNGLSTDTOTETSSITSESSSSGSGEPPALPSKLE 694  
 Db 481 SDMPRSGIYDSSVPSSELSPLNGLSTDTOTETSSITSESSSSGSGEPPALPSKLE 540  
 QY 695 SSGSKADLCGRSTYDELHVAAPL 718  
 Db 541 SSGSKADLCGRSTYDELHVAAPL 564

## RESULT 2

hypothetical protein Y64G10A.e - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C:Accession: T27282  
 R:Ainscough, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20336

A:Accession: T27282

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-846 <WIL>

A:Cross-references: EMBL:AL110498; PIDN:CA854470.1; CESP:Y64G10A.e

A:Gene: CESP:Y64G10A.e

A:Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3

C:Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e

Query Match 4.5%; Score 170.5; DB 2; Length 846;  
 Best Local Similarity 21.4%; Pred. No. 4.1e-05;  
 Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;

QY 64 QYACHDOAVTILSPGALGIEFLKGFVILEELKSGROCOQLIKDKPKOLNSPFRKG 123  
 Db 294 QY-CPEETEVRLLDSS---GIVMLQSAITIDELRTE-----IINGRPVQGF 338  
 QY 124 MESQPLNKKPFYFVYVPPPSIKNESNHYFFFRACOLLLOPNLAC-KPFWKPR 182  
 Db 339 ---NFTDIELDTOLIPSVIPESABD-----GRC-LCVTENGCSCLAAOKPV 382  
 QY 183 NLNISQSGSDMOVSFDIAPNFGFRFFLYLKLHKGPKRKTCKOBTETTSCLLONV 242  
 Db 383 KLT-----RIEKPATSN-----QTESDGAEDKEDITHY----- 415  
 QY 243 SPQDIYIELVDYTTTRVKG-YALKPVHSPWAGPINAIVTVPILVWISAFATL--FTVM 299  
 Db 416 -----MHYTA-----ITGGAITAILFSLVSCAGLCKYKFE 445  
 QY 300 CRKQOENYSHLDESESYTAAIPRLPRPRKVFICYSSKDGQNNVYVQCFAYF 359  
 Db 446 NKKKASNT--HLLNPAFS-HSGSIPL-ILKQISVLIVY-SHDSQAHEAVLAFAPL 500  
 QY 360 LQDFGCEVALDWFSLRCOREWYTIQIHESQPIIVVCSKMYFDKKNYKHGG 419  
 Db 501 LRDVFNVLHVDWDEDDI-EENRAEYINSSIVRANKVLIINSIG-ATP---RTVFHQ 555  
 QY 420 GRSGSGELFLVNSAIAELKQACQSSAALSKEFNAVTFDYSCEDV--PGILDISTY 477  
 Db 556 -----EPAEITGTGRD-----VIFDMQCEALQHPVCYSCHFYSI 591  
 QY 478 -----RLMD-NLPOLSHLSHSDGLQPGQORTQGSRRNYFSKSGSLYVAI 525  
 Db 592 TNPKYVFPPIVRLQYSIP---NSLMTMTALTTEQARPEQLAGFNQVFAR---LQAAI 644  
 QY 526 CNKHQFIDEEDPWFKEK-----QVFPFPPPLRYR----- 554  
 Db 645 SRLANYIESDPQWENTHVRVTRVSELAHNIVPL-PPSLKRVVEDAAGQMETLPI 703  
 QY 555 EPVLEK-----DSGLVLDVMCKPGPESDFCLVAAVLGATGPADESQES 601

Db 704 DELKEFAAKRDLVEVLDSEVDKLLDVKCAPG-----INVEPTEVLEPAEPNKE 758  
 QY 602 QHGGLDQGEARPALDGSAA---LQPLL-HVKAQSPDMPRDGIYDSS-VPSSELS 654  
 Db 759 ARED-EEEDVDQSVESQATREELQRLIVH-----KDMNEDSGNLDSATYSGDPS 809

## RESULT 3

T30113

hypothetical protein F56D1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T30113

R:Chisoe, S.; Wilson, R.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F56D1.

A:Reference number: Z20737

A:Accession: T30113

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-718 <CHI>

A:Cross-references: EMBL:U39997; PIDN:AAA81100.1; CESP:F56D1.2

A:Gene: CESP:F56D1.2

A:Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3

C:Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2

Query Match 3.3%; Score 126.5; DB 2; Length 718;  
 Best Local Similarity 20.6%; Pred. No. 0.1;  
 Matches 89; Conservative 68; Mismatches 165; Indels 111; Gaps 20;

QY 280 VAITVPLVVISAFSA-----TLFTVMCKKQOENYSHLDESESYTAAIPRLPRLP 333  
 Db 375 IAVVLLIILIIIVLAVTGFGVILWROKVRSEVRNI-----ALTE 413  
 QY 334 RKPFVLCYSSKDGQNNVYVQCFAYFLQDFGCEVALDWFSLRCRGQREWYVIOKIE 393  
 Db 414 FYKVMIVTAD-DNDLEHTDCVKLVENLNCASCDPVFLEKLITAEQIVPSRMLVQISS 472  
 QY 394 SPTILVCSKMYFDKKNYKHGGSGCKGELFVAVSAIAEKLPAQKSSAALSK 453  
 Db 473 LKFIIVYSDCAEKLITAESETHQIVQARPPADLPQPAKEMI---INDATHPPARK 529  
 QY 454 FIATYDFSCEDVP---GILDLSTYKRLMONLPOLCSHLHSRDLGQEPQORTGSR 510  
 Db 530 YAVVRFNYS--PHVPPNMLIILNLP-FILPEQFAQLTAFILHVEH-----TERA 575  
 QY 511 NYFRSKSGRSY---VAICMHQFIDEEDPWFKEQFVP-----PHPPPLATREPVLEKF 561  
 Db 576 NYTOISEAQIHEWNLCAKRNMSFFVRNPWLETFRWKPKDELAALH---LKRQSPVIVPI 632  
 QY 562 DSGVLNDVMCKPGPESDFCLVAAVLGATGPADESQESQSGGLDQGEARPALDGSAA 621  
 Db 633 QT-----EED---RIAAISIKYINLVPPQALVDSO-----DED 663  
 QY 622 LQPLLETVKAQSPDM---PRDSGIYDSSVPSSELSPLNGLSTDTOTETSSITSESSSS 679  
 Db 664 LQP--HASHQNPILILPPQCG-----PDSO-----SDSESSESSESSESDNE 706  
 QY 680 GLGEEPPALPSK 692  
 Db 707 G---EDPKTIIVK 716

## RESULT 4

T09081

telomere-associated recoQ-like helicase - smut fungus (Ustilago maydis) (fragment)

C:Species: Ustilago maydis (corn smut)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-May-2000

C:Accession: T09081

R:Sanchez-Alonso, P.; Guran, P.

Genetics 146, 1043-1054, 1998

A:Title: Organization of chromosome ends in Ustilago maydis: recoQ-like helicase motif

A:Reference number: 216557; MUID:98198830; PMID:9539423  
 A:Accession: T09081  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-757 <GAP>  
 A:Cross-references: EMBL:AF030885; NID:92642221; PID:92642222  
 A:Experimental source: strain FB2  
 C:Genetics:  
 A:Gene: UTASrecQ  
 C:Keywords: DNA binding

Query Match 3.19; Score 117; DB 2; Length 757;  
 Best Local Similarity 20.49; Pred. No. 0.64;  
 Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;

QY 233 ETTECLQNVSPGDYIIELVDVITRKVMYALPVSFWAGPIRAV---ATVPL-- 286  
 DB 77 ETTILPTVALRANNAKLQVNN---IRYHWQP--GSKAIPVLVSTEAATLAKKE 131  
 QY 287 -----VVISAFATLTVCKRKQENIYSHLDESESESTYALP----- 327  
 DB 132 YANRLQQLDRIVIDCHULTASYSRSMQLAWHRVDVETQVTLATLPIPEDA 191  
 QY 328 ---REKLPRPKV-----LCTSSKQGNHNVVQCF--AYLQDFCCCEVALDNEDF 376  
 DB 192 FISHKLTPLIVRESTNRSLCTSVTAHRMSGTCTDAVRVD--BCARTDIN--- 246  
 QY 377 SLREGQREWIQKIHESQFIYVCSKGMKFEVDK-----KNYKHGGGRGS----- 423  
 DB 247 ---NGQD-----RIIVCTTS--KELVARLAEMLGCAATSESSSEADKAALIQ 290  
 QY 424 ---GKGLPLVAVGAIKELQKQSSNAALSKEFIANTFYDSCEDVPGIIL--DLSTKY 477  
 DB 291 DWICGKSPVYATSA-----LVGDFYFHFVFIHLGPDLLDF 331  
 QY 478 -----RLNMLPQLCSHLSDHGLQEPQHTQGRSRNFRS 515  
 DB 332 SQESGRAGRDGPAESILLAGPQDDRAP--ASGKASSAEKGVAPG---ADKEAMQLYRS 387  
 QY 516 KSGSLYVAICNNHQFIDEEPDMFEKQVFPFHPPLRYREPLVEKEDSLVINDVMCKPG 575  
 DB 388 RK---YCLRGVLSQLLDQSDW-----RCKMEGQQLCSVC 419  
 QY 576 PESDFCLKVAEAVLQAGPADSOH---ESQHGGLDQCEARPALDGSAAALPILLETYKAG 632  
 DB 420 PGHFF-----QARGPGQFHTAPAQAGDPSTQGRSPSMEGSS--HPSNH----- 463  
 QY 633 SPSPMDPRDGIYDSSVPSSSE--LSLPLMEGLSTDTQETSSLTSEYSSS---SGLGEEPPRA 688  
 DB 464 -----GSSHPSSGSHSPSHSGSHPSHSGSS--HPSHSGQHQGRKQKQPD 510  
 QY 689 LPSK 692  
 DB 511 PPSE 514

## RESULT 5

F83781  
 transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus ha  
 C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 A:Accession: F83781  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000.  
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: AB3650; MUID:20512582; PMID:11058132  
 A:Accession: F83781  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-901 <STO>  
 A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA04773.1; GSPDB:GNOC  
 A:Experimental source: strain C-125  
 C:Genetics:

A:Gene: BH1054

Query Match 3.08; Score 116.5; DB 2; Length 901;  
 Best Local Similarity 19.68; Pred. No. 0.9;  
 Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY 26 ASRNSGLYNTFTKDYDNCYTLNVPVKHVIADQNTTISQY--ACHQVAVVITLSPGALGI 84  
 DB 333 ALKESGL-----PLPKTLIADAGTSGESNTVAMADELFTLIPS----- 371  
 QY 85 EFLKGRFVILEELKSEGR-----OCQOL--ILKDPKOLNSSFARKTGESQFLNKKF 134  
 DB 372 ---HTFR--OEKRSFAKRFPHNRCDETDDVTWCPNQKVSFKRYKRTDY--GY 423  
 QY 135 ETDYEV-----KVVPF--PSI-----KNESYHPEFETRACDLLODNLACKPFKPR 182  
 DB 424 ARDEKYTECESCGCFPPCTKARGNRQVHNPVY-----ELKAKHQKLLK 471  
 QY 183 NLNLSQHG-----SDMQVSTFHAPHNFRPFRFYLYLKHGEGFKKTKQBOTET 234  
 DB 472 ---SEGRTLQKKTIVESYFHVQKQZGFRRLHGRK----- 507  
 QY 235 TSCLLQNVSPGDYIIELVDVNTTRKVMYALPVSFWAGPIRAVAVITPLVWIS--AFA 293  
 DB 508 -----ESVHIELGIVLAHLNR 524  
 QY 294 TLPVWCRRKQOENIYSHLDESESESTYTAALPRERLPRPKVFLCYSSKDGQNHMVV 353  
 DB 535 KRATVDRRSKEPKNTQNKREN-----RIKRF-----SRFTVL 558  
 QY 354 QCF---AYELQDFCCCEVALDNEFSLQCEQRENV-----IOLIHESQFIYVCSGKMK 406  
 DB 559 RCWDSPPFIKSDGQYASPALFD--KLREGGENHIEVDLSKTYRNRQV--KGIN 612  
 QY 407 YFDKKNYKHKGGRSGSGELFLVAVSAI-----AKLQKQKSSAALK 453  
 DB 613 MFEKQEMVLLGPGNAGKSTTSMISSLIQPTSGDVLKIGKSIHRSKAINSLGVVPQ 672  
 QY 454 FIAYTFDYSC-----GDVFGILDLSTKYRLMNLQPLQCSHLSDHGLQEPQHTROG 507  
 DB 673 EIAYTHDLTARENLAFFGKIYGLKGEELKHR--MESTLQLV-----GLEE--RQN 718  
 QY 508 SRNRYFSKSGSLVAICNNHQ---FIDEEP 536  
 DB 719 DRVHTSGGKRLNIAVALLHEPELIINDEP 750

## RESULT 6

T17212  
 hypothetical protein DKFP434P211.1 - human (fragments)  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 A:Accession: T17212  
 R:Poustka, A.; Klein, M.; Neues, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18723  
 A:Accession: T17212  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-488; 489-535 <POD>  
 A:Cross-references: EMBL:AL117401  
 A:Experimental source: adult testis; clone DKFP434P211  
 A:Note: the cDNA sequence contains a -1 frameshift near codon 488  
 C:Genetics:  
 A:Note: DKFP434P211.1

Query Match 2.94; Score 110; DB 2; Length 535;  
 Best Local Similarity 23.58; Pred. No. 1.4;  
 Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;  
 QY 439 KLRQAKSS--SAALSKEFTAVTFYDSCGQVPGI-----LDLSTKRLMDLQPO 485  
 DB 103 RYNTSOTSTWTSCTNRNNAISSSYSTGGLPQLARBRGPASSHSCQLTSSSKYTSERDPO 162



QY 486 LCSEHSRDLQGE--PCQHTGSGRNRYFRSKGRSLYVACNMHOFIDEPWFKEQF 543  
DB 163 AVSGHTQCEKAADITAPGQTLT--LRNDSSTSEASRP-----STHKE-----PLLPRRG 210  
QY 544 VPPE-PPPL-----RYREPVEKFDGLVNDVM--CKPESDFCLVEAA 587  
DB 211 EPLMLPPLEGLRYVTVEDLDREKAAPORINSALOVDEKATSDCRPSRSH--TLSIL 267  
QY 588 VLGATC-PADSHSORSGLDQGEARPAIDGSAALQPLHIVKAGSPDMP-----RD 640  
DB 268 ATGASGLPAVSAPVS-----MDAOTHSQCGLGLDPLASA--AGVSTAPMSGKKHRP 321  
QY 641 SG-IYDSSVPSELSPLMBGLSTQDTSTSLTSYSSSSSGSGEPEPALPSKLLSSG 697  
DB 322 PGFLFSSDP-----LPATSDSQDSAQVTSLI-----PAPFPASMDAG 361

## RESULT 7

149239  
vesicle transport protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I49239  
R:Telam, J. T.; McIntosh, S.; James, D. E.  
J. Biol. Chem. 270, 5957-5963, 1995  
A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neurons  
A:Reference number: 149239; PMID:95197608; PMID:7890715  
A:Accession: I49239  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-592 <RES>  
A:Cross-references: EMBL:U19521; NID:9642027; PIDN:AAA69913.1; PID:9642028  
C:Genetics:  
A:Gene: munc-18c

Query Match 2.9% Score 110; DB 2; Length 592;  
Best Local Similarity 18.5%; Pred. No. 1.6;  
Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;

QY 286 LVVISAFATFTVCRKQKQ-----ENYSHLDESSSTYTAALPRELRPRK 336  
DB 34 IMLDFTKLLSSCATDLEEGITVENIYKRPVOMKALYF-----ISPTK 86  
QY 337 VFLCYSSKQGNHNVQCFAYLQDFC-----GCE----- 367  
DB 87 SVDFLRDQSGSEKKYKAAIYTFDQPSLNFNFKASCSIRCKEINISFPOESO 146  
QY 368 -VALDLWEDFSIC-----REGQREWIQKHESQFIIVVC-----SKGNY----- 407  
DB 147 VITLDVDAFYCYSPSPNSASKEVMEAAEQ--IVTVCATLDENPGVYKSKPLDNA 204  
QY 408 -----FVDRKK--NYK--HKGGRSGKGLFLV-----AVSAIAEKLRQAKSSAALS 452  
DB 205 SKLAQLVEKKLEDYKIDEGGLKGTQSQLLIDRGDPVSTVLEL----- 252  
QY 453 KFTAVTFD-----YSCG-DVPGIL-----DLSTKR-----LADNLPLCSHLH 491  
DB 253 TFOAMAYDLLPIENTYKTKDKEAVELEDDDLWVRVNRHHAIVLEIPLMKETS 312  
QY 492 SRDGLQEPGHTROGGRNRYFRSKGRSLYVACNMHOFIDEPWFKEQFVFPHPPL 551  
DB 313 STR-----KATEGKTSLSALTQLMKMPHFRLQSKOV-----HL 348  
QY 552 RYREPVEKFDGLVNDVMCKPESDFCLVE 585  
DB 349 NLAECDMKNFLNIEKCKTEQDLAIGTDAEQVRKDSMLVLLPVLL--NKNEDNCKIR 406  
QY 586 AVNLGATGAPDSQHSQHGGLDQGEARPAIDGSAALQPLHIVKAGSPDMP--SGIT 644  
DB 407 AVLYIFGLNGTTEEN-----LDRLIHNVKIEDSDSMIRNWSHLG 446  
QY 645 DSSVPSELSPLMBGLSTQDT 666

DB 447 VPIVPPSQAPLPRKDRSAET 468

## RESULT 8

T04661  
hypothetical protein F8D20.70 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 24-Nov-1999  
C:Accession: T04661  
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mew  
submitted to the Protein Sequence Database, July 1998  
A:Reference number: 215381  
A:Accession: T04661  
A:Molecule type: DNA  
A:Residues: 1-917 <BEV>  
A:Cross-references: EMBL:AL031135  
A:Experimental source: cultivar Columbia; BAC clone F8D20  
C:Genetics:  
A:Map position: 4  
A:Introns: 13/3; 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3;  
A:Note: F8D20.70  
C:Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70

Query Match 2.9% Score 110; DB 2; Length 917;

Best Local Similarity 18.1%; Pred. No. 3;  
Matches 154; Conservative 124; Mismatches 281; Indels 292; Gaps 37;

QY 24 GPASR-----NSGLYNITFKYDNCNTYTLNPKVHV---IADAQNI--TISQACHDQVA 72

DB 148 GRASRVYIGSSSSNSQVLLNEQETETNKLGLHVFSEPCADMEMLIADVNEQSKRQDF 207

QY 73 VTILNSPGALGI--EFLKGRVILEELBSGRQOOLILKPKOLNSFKRTGHESQP--- 128

DB 208 LFLVGLKGRVYATDDYMIKYLIOQSKSPSLPKETVTVKLPFSOSSITVGLFNPFSH 267

QY 129 FLNMFETDY-----FVWVPPFPKRNESN---YHFF-----FTRACDLALQFDNL 173

DB 268 LLNLSDI--DYAQLAKDAVPPFETVVPKSSRAHFGFTKVKVNIITGHCDDGTISVMD 326

QY 174 ACK-----PPMKPR-NLNTSOG-----SDMOVSPDHAPENFGPFYFLRYKL 215

DB 327 TCSFPLVFLKQIDQDVSRSNAALTAHYDSNLSLAVSGDHNGVLYRKPEPILT 386

QY 216 KH-----EGPFR-----KTKQDQTTTETTCILQNVSP-----GDYIELVD 254

DB 387 ENSFIPQGLKGNHIVQSVYIKLGTSTICQSKNSKHLATGSDGSRGLVAVID- 445

QY 255 TNRTRVMYALKPVHSPWAGPIRAVAITVPLVVISAFATLFT----- 297

DB 446 -----ALTPEV-----LQVSLVDIEANVLYTKHIASDICPGIISLOPE 484

QY 298 -----VMCRRKQENIYSHLDESSSTYTAALPRELRPRKPFVFLCYTSKQO 347

DB 485 SCIVQGFENLVVWMDSDVFA-LDSDTGNMIGTNMKPK-----KPKVLTWQILDCK 538

QY 348 NEMVTVQCFATFDQFCGEVALDLWEDFSICREGQREWIQKHESQFIIVCS----- 402

DB 539 -----ODTSG-----NGFTSRES-----TVEEISIRQPSVLLVCEKAIY 573

QY 403 -----KGMKYFVDRKKNYKHG-----GGRSGKGLFLVAVSAIAE-----KLR 441

DB 574 IYSLAHVYGVGVKYLHKHKKFFSSPSCASASTFYGTSGVG---LTLVFTDGTVEIRSLPELS 630

QY 442 QAKQS-----SSAALSFAVIFYDSCED-----VPGILDLSYRLMDNL 483

DB 631 QLKQTSIRGETTSYSPKNSLPETITASWDGDLVWNGDDELIVSSVLPQKETFRLVESH 690

QY 484 POLCSLHSRDRGLQEPGHTROGGR-----NYPKSGSLVAVACNMHOFIDEPED 537

DB 691 -----NRVTKONSVCHEGIITSSSPREKSMFGSVFTKSKTKTTTPESSKETIEELSK 746

QY 538 WFEQFVPF-----HPPPLRTPVLEKFPDGL 565



Db 747 IFSTANFNNVNSREINTIYVEDEELDDIDDHPNCOOQEPKQGLISGL 806  
 QY 566 -----VLNDVCKCPQSPDCLVAVLGCATGADSOHESQGGGL-----DO 608  
 Db 807 STOKMAREFNFKLQMAAKNEKSVV-----TNDKHEKNGATVQIKKKYGFRTSDE 862  
 QY 609 DGEARPDGSAALQPLLETVKAGSPDMPSDGIYDSSVPSSELSPLAEGLSQTQET 668  
 Db 863 MGAARHA-----QSKLAD-----NLKLGISLRTTEM 890  
 QY 669 SSITESVSASS 679  
 Db 891 EDATKSFSSA 901

## RESULT 9

837627

protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human

C:Species: Homo sapiens (man)

C&gt;Date: 19-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 04-Feb-2000

C:Accession: S37627

R:Bohme, B.; Boltrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Strebhardt, K.; Ruebs

Oncogene 8, 2857-2862, 1993

A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.

A:Reference number: S37627; MUID:93390963; PMID:8397371

A:Accession: S37627

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-998 &lt;BOE&gt;

A:Cross-references: EMBL:X5208; NID:q406867; PIDN:CAA53021.1; PID:q406868

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat

C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki

P:631-899/Domain: protein kinase homology &lt;KIN&gt;

P:639-647/Region: protein kinase ATP-binding motif

P:922-988/Domain: SAM homology &lt;SAM&gt;

Query Match 2.8%; Score 109; DB 2; Length 998;

Best Local Similarity 18.9%; Pred. No. 4.1;

Matches 157; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

QY 1 ADTCGRMKAARPRIC-----VANEGVGA-----SRNSG-----LYNITFY 39

Db 268 ACTCATGHEPAKESOCRCACPGSYKAKQGGCLPCPNSTTSPAASICTCHNNFYA 327

QY 40 DN-----CTTILNPVKRVIAADQNTITISQYACHDOVAVTILMS-PCALGIEFLKGRV 92

Db 328 DSDSADSACTTVSP-PRGVISNV-----NETSLILEWSEPDGLGVRODLLYNV 375

QY 93 ILLEELKSEG-----RCCOOLILKDPKOLNSFKRTGMSQPLANKKETDYFKVYVPPS 147

Db 376 ICEKHGAGGASACRCDNDVFFPRQLGLSEPRVHS-----HLIARTYTFEVAQVNG 430

QY 148 IKNESNYAPFFTRACDILLQDMLACKPFWPRNLNISQSGDMQVSDPHAFNFR 207

Db 431 VSKSPPLPRYAIVNTTNOAPSEV-----PTLRHSSSGSSILTSWAPPENPG-- 481

QY 208 FTLNPKLKHGEPF-KRKTKOEQTETTSCLLQNVSP-GDYIIEVDNTNTRKVMHYA 265

Db 482 -VILDYEMKY---FEKSEGTASTVTSQMSVOLDGLRDPARYVQV-----BARTVAGV 532

QY 266 -LKPVH---SPWAGPIRAVAITVPLVVISAPATL-----PTVMCKKQOENIYSH 311

Db 533 QYSPAEFETTSERGSAOQLOEQLPLVGSATAGLVAVVAVVIAVCLKQRH----- 587

QY 312 LDEESSESTTAAIPRERLRPRKVFCLCYSSKQGNHNVQCFAYFLODFC-GCEVAL 370

Db 588 -----GSDSEYTEKL-QOYIAPGMKVIIDPFTEDPN--BAVREFAEIDVSCVKIERY 639

QY 371 DLWEDFSLCRGOREWYIQIHESQFIIVVCSKGMKYFVDKKNYKHEGGGSGSGKELEF 430

Db 640 GAGEGGEVCR-----GLKQPCRGREVE- 661

QY 431 YAVSAI---AEKLQAKOSSAALSFIAYFDISCBGDPVGILDS---TKYR----- 478  
 Db 662 VAIKTLKVGTTERRORDFLSASLNGOF-----DIPNIIRLEGVYTKSRVAIL 710  
 QY 479 --LMDNLPQLCSHLHSRDRGLQEPQGT-----RQGSRRNY-FRSKSGRS 520  
 Db 711 TEFKENC-ALDSFLRLND-----GQFTVTLQVGMIRGIAAGAKYLSMMYVHRDLAARN 763  
 QY 521 IYV---AIC-----NNHQFIDEEDNFEKQVFFHPP-----PLRTREP---VLEKEDS 563  
 Db 764 ILVNSNLVCKVSDFGLSRFLDQPS-----DPTTSSLGCKIPIRWTAPEAIAYRKETS 817  
 QY 564-----GLVNDVMCKCPQSPDCLAVEAAVLGATGADSOHESQGGGLDQDGEARAL 616  
 Db 818 ASDVMSYGIYMEVMS-----YGERPTWMSQDVINAVEQDYRLPPPM 861  
 QY 617 DGSALQPLLETVKAGSPDMPSDGIYDS-----SVPSSELSPLMEGLS 662  
 Db 862 DCPALHQLMDQWDRMLRPFQSVIVNTDLKLIRNAASKVYASQSGSQPLDRTV 921  
 QY 663 TDOTETSLTESYSSSGIGEEPPALPSKLLSSGSKADLCGRSYDEL 712  
 Db 922 PDYTTFTTVDGMDLAIK-MGRYK-----ESFVSAGFASFDLVQAQMTAEDL 965

## RESULT 10

I49071

protein kinase - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999

C:Accession: I49071

R:Ruiz, J.C.; Coolon, F.L.; Robertson, E.J.

Mech. Dev. 48, 133-164, 1994

A:Title: Identification of novel protein kinases expressed in the myocardium of the d

A:Reference number: I49071; MUID:95200798; PMID:7893599

A:Accession: I49071

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-938 &lt;RES&gt;

A:Cross-references: EMBL:U11493; NID:g595418; PIDN:AAA67925.1; PID:g595419

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea

C:Keywords: ATP; transmembrane protein

F:571-839/Domain: protein kinase homology &lt;KIN&gt;

F:579-587/Region: protein kinase ATP-binding motif

F:862-928/Domain: SAM homology &lt;SAM&gt;

Query Match 2.8%; Score 107.5; DB 2; Length 938;

Best Local Similarity 19.3%; Pred. No. 5;

Matches 152; Conservative 115; Mismatches 271; Indels 251; Gaps 42;

QY 1 ADTCGRMKAARPRIC-----VANEGVGA-----SRNSG-----LYNITFY 39

Db 205 ACTCATGHEPAKESOCRCACPGSYKAKQGGCLPCPNSTTSPAASICTCHNNFYA 264

QY 40 DN-----CTTILNPVKRVIAADQNTITISQYACHDOVAVTILMS-PCALGIEFLKGRV 92

Db 265 DSDSADSACTTVSP-PRGVISNV-----NETSLILEWSEPDGLGVRODLLYNV 312

QY 93 ILLEELK-SEG-----RCCOOLILKDPKOLNSFKRTGMSQPLANKKETDYFKVYVVP 144

Db 313 ICEKHGAGGAGGACRCDNDVFFPRQLGLSEPRVHS-----HLIARTYTFEVAQ 367

QY 145 FSIKNESNTHPFFTRACDILLQDMLACKPFWPRNLNISQSGDMQVSDPHAFN 204

Db 368 VNGVSGKSPFPPIRYAIVNTTNOAPSEV-----PTLRHSTSGSSLTSWAPPEN 420

QY 205 GPRFFTLTKLKHGEPF-KRKTKOEQTETTSCLLQNVSP-GDYIIEVDNTNTRKV- 261

Db 421 G---VILDYEMKY---FEKSAIATSTVTSQMSVOLDGLQDARYVQV-----BARTVA 469

QY 262 -----MYALKPVHSPWAGPIRAVAITVPLVVISAPATL-----TLFTVMCKKQOENI 308

Db 470 GYGOTHPAEFETTSERGSAOQLOEQLPLVGSATAGLVAVVAVVIAVCLKQRH-- 527

309 YSHLDSESSSTYTAALPRERLRPRKPVFLCYSSKQDQHMNNVOCFAIFLQDFC-GCE 367  
 528 -----GPDABYTEKL-QQYIAPGMKVVIDPFTYEDPN-EAVREPAKEIDVSCVKIE 576  
 368 VALDWDPSLCRQREWMVQIKHESQFIIVVCSKGMKYFVKNNYKHKGGSGSGE 427  
 577 EVIAGEGEVCR-----GLKLPGRRE 599  
 438 LEIVANSAI-----AKLQKQSSAALSKFTANTFYDSCGDPGILDL-----TKTR----- 478  
 600 VVVAITLAVGTENQRDFLSASMGOF-----DHPNIIINLEGVVTKSPV 647  
 479 -----LMDNLPOLCSHLSDHGLQEPGQHT-----ROGSRNRY-FRKS 517  
 648 MILPEMENC-ALDSFLIND-----GOFTYIOLVGMNIAAGMKYLSNNYVHRDLA 700  
 518 GRSLTV-----AIC-----NMHOFIDEPWFKEOF-----VPPH-----PPPLRYREPYLE 559  
 701 ARNIVNSNLVKVSDGSLRFLRLEDDPS--DPTTSSLGKIPIRMTAPEPIAYR----- 753  
 560 KFDV-----GLVNDVCKPGPESDFCLKVEAAVILGATGADSDHSHQGGILDGDEA 612  
 754 KFDASDVWSYGVVMEVMS-----YGEOPYNMSNQDDINAVQDYRL 797  
 613 PPAIDGSAALOPILTVTAGSPDMRPSGIYD-----SSVSSLSLPL 657  
 798 PPMDCPTALQKMSCWVRDNRNLPKFSQIVNTLDKLRMAASLKVYASFG-MSQPL 856  
 558 MEGSLTDQT 666  
 857 LDRTVPDYT 865

RESULT 11

T13960  
 beige.protein homolog - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T13960  
 R:Wori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.  
 submitted to the EMBL Data Library, November 1998  
 A:Description: Deletion in the beige gene of the beige rat due to recombination between  
 A:Reference number: Z17837  
 A:Accession: T13960  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-3788 <MOR>  
 A:Cross-references: EMBL:AB020019; NID:d1241953; PID:d1035670; PIDN:BAA34688.1  
 A:Experimental source: strain DA; spleen  
 C:Genetics:  
 A:Gene: beige

Query Match 2.84; Score 107.5; DB 2; Length 3788;  
 Best Local Similarity 19.78; Pred. No. 39;  
 Matches 142; Conservative 93; Mismatches 258; Indels 229; Gaps 38;  
 16 LCVAHEGVG---PASR-----NSGLYNTFYKDNCTTYLNPVKGKHVIAADQNTISQYA 66  
 658 LCGAGPGCLGPSYKFGILPSSGSEDFLWDALEYQNFIPQE--DRLEHTQIASHI 715  
 67 CH--DOVAVTILSPGALGIEFLKGFVILELKSEG-----ROCCQILMDPKQLNSFK 120  
 716 CNLIQKGNIVQW-----KLYNIFNPVLRGVYELVHHCQQLSI-----TSA 757  
 121 RTGMSOPFLNMKFEF-DYFVKVVP-----PPSIKN-----ESNY-----HPP 157  
 758 QTHSSQLKQLVQVQLVQLKTLPIILKSRVIRDLSCSNVNHIELNLDGIRSHSL 817  
 158 -FFETRADCLLOPMLACKFWKPRNINISQSDMOVSFDHAPHNFRGFYLYLK 216  
 818 KAFETLIVSLGQKKRAVPGV---DGLDIOQLSLSLV----- 853

217 HEGPFRKTKCKOBQTTTSCILQNVSPGDYIIELVDDTNTTRKVMHATAPVPSWAPG 276  
 854 --GFSLHK-----QOASTDPSCLRK-----FYASLRDTPFKRKTVHQ----- 890  
 277 IRAVATVPLVVISAPATLFTVMCRKQKENIYSHLDSESSSTY---TAALPRERLRPR 334  
 891 -DAHINTINILCVAF-----LCYSKESADRESAN-ESEDTSGYSTASEPLSHMLPR 942  
 335 PKVFLCYSSKQDQHMNNV-----OCFAIFLQDFCCEVALDILWEDFSLCRCGQRENV--I 388  
 943 LSL-----ENVLPSECLH-----ADIN-----SMCR-----NIYML 972  
 389 OKHESQFI-----TVCSKGMKYFVKNNYKHKGGSGSGKGELEF-----LVASIAIE 438  
 973 NSYFQKFERLGGFYVCHE-LIFMIIQKLFHSHTEDQGRQGENSYVKNKNOGLAMRISQPEM 1031  
 439 KLRQAKQSSAALSKFTANTFYDSCGDPGILD-----LSTK----- 476  
 1032 ILKEDVSSSTAPEPGFLKKSADRVSELSQHMPLTSAEQILATKSGIPGEATFMANOES 1091  
 477 -----YRLMDNLPOLCSH-----LHSDRDGLQEPGQHTROGSRNRYFKSGRSLYVAICNKH 529  
 1092 CIGSIRLLSGLAICHSARASQOKMELEPSQ-----DNFEKQFVPPHPPPLATREPVLKFTDGLVNDVCKPCPS 578  
 530 QFTDEP-----DNFEKQFVPPHPPPLATREPVLKFTDGLVNDVCKPCPS 578  
 1137 DILSQSKVAETELAPLFDALLRVALGNHSADLPDQGTIVTEKSHPS---EVLVSQPDPS 1193  
 579 DFLCKVAAVILGATG-----PADSQHSHQGLDQGEARPAIDG-SAALOP--LLHTVK 630  
 1194 EEAEDSQCCSLKLLGEEGYEADSENPDGTDQDGVFLPFAEGFSGSIVPNLLES 1253  
 631 AG 632  
 1254 HG 1255

RESULT 12

T42730  
 Bassoon protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T42730  
 R:Dieck, S.; Samartti-Villa, L.; Langanaese, K.; Richter, K.; Kindler, S.; Soyke, A.; W  
 J. Cell Biol. 142, 499-509, 1998  
 A>Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively local  
 A:Reference number: Z22249; MUID:98345363; PMID:9679447  
 A:Accession: T42730  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3942 <DIE>  
 A:Cross-references: EMBL:U17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810  
 A:Experimental source: strain 129 SVJ  
 C:Genetics:  
 A:Map position: 9F1  
 A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1  
 A:Note: bassoon  
 C:Function:  
 A:Description: may be involved in cytomatrix organization at the site of neurotransm  
 A:Note: component of the presynaptic cytoskeleton  
 C:Keywords: coiled coil; zinc finger

Query Match 2.84; Score 107.5; DB 2; Length 3942;  
 Best Local Similarity 19.18; Pred. No. 41;  
 Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;  
 481 DNLPLCSHLSDHGLQEPGQHTROGSRNRYFKSGRSLYVAIC-----NMHOFIDEE 535  
 3535 DTCQFCS-----SHSMFDQVQEHVQDGRAHAYKRESGYNLDSDHSCVSDSEAVHLQEE 589  
 536 PDWFEKQFVPPPPPLRYRE-----PVLEKF-----DSGLVNDVCKPCPS 575  
 3590 TDWFDK---FRDARSDFRHHGHTVSSQKNGKPARHSYHDYDPEPEGLPHD---EAG 3643

QY . 407 YFVDKKNYKHKGGRSGKGELFLVAVSAIAEKLROAKOSSAALSKFIAVYFDYSCEGD 466

dp 1038 -----YBETITKCVQSSATAPDICEI  
||| : ||  
|||

nk 1038 -----YBETITKCOVSSATAPDICEI



GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:08:53 ; Search time 14.5787 seconds  
(without alignments)  
2042.709 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_36\_753

Perfect score: 3829

Sequence: 1 AOTCGWMAAARPLCVAN.....CTADLCRSYIDELHAVAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	310	8.1	866	1 I17R_HUMAN	Q96f46 homo sapien
2	306	8.0	864	1 I17R_MOUSE	Q60943 mus musculus
3	135.5	3.5	502	1 I17S_HUMAN	Q9nmr6 homo sapien
4	126.5	3.3	718	1 YS02_CAEEL	Q10128 caenorhabdit
5	110.5	2.9	499	1 I17S_MOUSE	Q94193 mus musculus
6	110	2.9	592	1 STB3_MOUSE	Q60770 mus musculus
7	109	2.8	998	1 EPB3_HUMAN	P54753 homo sapien
8	104	2.7	1462	1 PTP6_DROME	P16620 drosophila
9	103.5	2.7	663	1 RGP2_HUMAN	P47736 homo sapien
10	102	2.7	859	1 ABR_HUMAN	Q12979 homo sapien
11	101	2.6	1275	1 GNRP_HUMAN	Q13972 homo sapien
12	99.5	2.6	794	1 2F12_MOUSE	Q60821 mus musculus
13	99	2.6	783	1 2F21_MOUSE	P20662 mus musculus
14	99	2.6	970	1 PS01_YEAST	P53550 saccharomyc
15	98.5	2.6	1050	1 EK5B_CHLPN	Q92797 chlamydia p
16	98	2.6	820	1 CTNB_TRIGR	P35223 tripeustes
17	97.5	2.5	1845	1 Z336_HUMAN	Q9u136 homo sapien
18	97	2.5	984	1 EPB1_RAT	P09759 rattus norv
19	96.5	2.5	746	1 ABL_HVAB	P05521 abelson mur
20	96	2.5	424	1 MK05_HUMAN	P45984 homo sapien
21	96	2.5	660	1 HT31_ARATH	P45986 arabidopsis
22	96	2.5	902	1 EPB3_XENLA	Q94796 xenopus lae
23	96	2.5	984	1 EPB1_CHICK	Q07494 gallus gall
24	96	2.5	1114	1 E2K3_MOUSE	Q9z2b5 mus musculus
25	95	2.5	828	1 CAN_DROME	Q11002 drosophila
26	95	2.5	933	1 PRGR_HUMAN	P06401 homo sapien
27	95	2.5	1036	1 AXOL_CHICK	P28685 gallus gall
28	94.5	2.5	351	1 EM14_CAEEL	P20271 caenorhabdi
29	94.5	2.5	770	1 GIT1_RAT	Q9z272 rattus norv
30	94.5	2.5	841	1 I563_MCNVS	Q69154 murine cyto
31	94.5	2.5	1011	1 M3K6_HUMAN	Q95382 homo sapien
32	94	2.5	984	1 EPB1_HUMAN	P54762 homo sapien
33	94	2.5	2044	1 SIF2_DROME	P91620 drosophila

34	94	2.5	2064	1 SIF1_DROME	P91621 drosophila
35	93.5	2.4	806	1 RMIL_CHICK	Q04982 gallus gall
36	93.5	2.4	807	1 RMIL_COTJA	P34908 coturnix co
37	93.5	2.4	901	1 A180_MOUSE	Q61548 mus musculus
38	93.5	2.4	915	1 A180_RAT	Q03140 rattus norv
39	93	2.4	429	1 EPC_RAT	P01855 rattus norv
40	92.5	2.4	347	1 SH33_MOUSE	Q62421 mus musculus
41	92.5	2.4	548	1 IDD_MOUSE	P98154 mus musculus
42	92.5	2.4	684	1 FBEL_CHICK	Q73775 gallus gall
43	92.5	2.4	830	1 JIP2_MOUSE	Q9ere9 mus musculus
44	92.5	2.4	993	1 EPB3_MOUSE	P54754 mus musculus
45	92.5	2.4	2314	1 PTP2_HUMAN	P23471 homo sapien

#### ALIGNMENTS

##### RESULT 1

I17R\_HUMAN  
ID I17R\_HUMAN STANDARD; PRT; 866 AA.  
AC Q96f46; Q04384;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17 receptor precursor (IL-17 receptor).  
GN IL17R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP TISSUE: T-cell;  
RC MEDLINE=98035683; PubMed=9367539;  
RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,  
RA VandenBos T., Zappone J., Painter S.L., Armitage R.J.;  
RT Molecular characterization of the human interleukin (IL)-17  
receptor.  
RL Cytokine 9:794-800(1997).  
RN [2]  
RP TISSUE: Uterus;  
RC Strausberg R.;  
RA Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
CC suggesting that additional components are involved in IL17-induced  
CC signaling.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- TISSUE SPECIFICITY: Widely expressed.  
CC -!- PTM: Glycosylated.

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EMBL; U58917; AB99730.1;  
EMBL; BC011624; AAH11624.1;  
DR Genew; HGNC:5985; IL17R.  
DR MIM; 605461;  
KW Receptor; Transmembrane; Signal; Glycoprotein.  
FT SIGNAL 1 31  
FT CHAIN 32 866  
FT DOMAIN 32 320  
FT TRANSMEM 321 341  
FT DOMAIN 342 866  
FT DOMAIN 810 818  
FT POLY-GLY 49 49  
FT CARBOHYD 54 54  
FT CARBOHYD 206 206  
FT POTENTIAL.  
FT INTERLEUKIN-17 RECEPTOR.  
FT EXTRACELLULAR (POTENTIAL).  
FT POTENTIAL.  
FT CYTOPLASMIC (POTENTIAL).  
FT POLY-GLY  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT N-LINKED (GLCNAC. .) (POTENTIAL).  
FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 225 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CARBOHYD 242 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CARBOHYD 265 N-LINKED (GLCNAC...) (POTENTIAL)  
 FT CONFLICT 367 V->A (IN REF 1)  
 FT CONFLICT 580 E->R (IN REF 1)  
 SQ SEQUENCE 866 AA; 96131 MW; 28330BED3303B0C9 CRC64;

Query Match 8.1%; Score 310; DB 1; Length 866;  
 Best Local Similarity 23.1%; Pred. No. 6.4e-16;  
 Matches 176; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 34 NITPKYDNC--TYLNVGKHEVITADANIT-----ISOYACHDQ-----VAVTILWS 78  
 DB 49 NCTVNSTCLDSDWTHP-----RNLTSPSPDQIQCHFAFTQOGLFFPAVHLEWT 99  
 QY 79 PGALGIEFLKGRVILBELKSGROCOOLILADPKQLNSFKRTGHSOPFLANKFETD 137  
 DB 100 LQTDASILTLEGAEISVLQATNERLCVR--FEFLSKLRHHRHRRFTSFHV-VDPDOE 156  
 QY 138 YFVKV--VPPPSIKNESYHPFFETRACDILLOPDNLACK-----PFWKPNL----- 184  
 DB 157 YEIVVHELPRIPDGNHQSKNPLVDCHEARKNVITPCMSGSLWDP-NITVETLEAH 215  
 QY 185 -----NISQSGDMQVSEDAHNGCFRFFYLHVKLKHGCPKRTCKQBOTTEYT 235  
 DB 216 QLRVSFTLANESTHQILISFFPMENHSCFEHMH-HIPAPRPEEFHQRNSVTILRNKL 274  
 QY 236 SCLQNVSPGDIILBLDDT---NTRKVMHVALPVHUSWAGPVRNAVITVPLVITSAP 292  
 DB 275 GCRHQVQVOTPFSSCLNDCLRHSAVSCPEMPDTPPEIDYMLPVVITFGSILLVG 334  
 QY 293 ALFTVYVCKRKKQOEIYSHLDESESSSTYTAALPRERLRPR-----KVFCLYSKDGON 348  
 DB 335 SVILLVCMTRWLAGGS--EKYSQDTYTDGLPVDLIPPLKPRKVIYISA-DHPL 390  
 QY 349 RMNVVCKFAFYFLQDPCGCEVALDWDLSLCREGQREWV---IQKHESQPIVIVCSKG 404  
 DB 391 YVDVVLFAQELLTACGTEVALDLLEQALISEAGVWTVGKQENVESNKIIVILCSRG 450  
 QY 405 MYIVDKNKYHKGG-----RSGGGEFLVAVSATAELKRAQKSSAALSKFIA 456  
 DB 431 TR-----AKWALLGKGVAVRLCDKPKVGDGLFTAMAMHILPFRK-----PACFGTIV 501  
 QY 457 VTF-DYSCREDVPGILSTYKRLMONLPOLCSHLHSDHGLQEPQHTQSG--SRNYF 513  
 DB 502 CYFSEVSCDGVDFLFGAARVPLADRFEEV--YFRQDLEMFPQGMHVRVSGDNIL 559  
 QY 514 RSKSGSLVAICNHQFIDEEPWF-----KQVFPFPPPLRIEPPVLEKFSGL 565  
 DB 560 RSPGQRLAALDRFDVQVHCDFWFCENLYSADQDAPSLDEEV-FEELPLPP-GTGI 617  
 QY 566 VLNDVCKKPGPSDFCLKVAEAVLGATGADSOHE-----SOHGG 605  
 DB 618 VKRAPLVRE-PCSQACLAIDPLVGEEGAVALKLEPHLPQPGAPQPLHTLVLAEEGA 676  
 QY 606 LDQDGEARALDGA--ALQ-----PLHVTAGSPSDMPROSGIDYSSVPSSELSLP 656  
 DB 677 LVAAVEGFLAAGAVRLAAGEACEAPILGSPGAG-----RNSVLF--LPVDPEPS 727  
 QY 657 LMELSTQDTQTSSTESVSSSGLGEERPPALPFLSKLSSGSKADLQC 705  
 DB 728 L-GSSTPMASPDLLPEVDR-----EHLEGIMLSLFLQSLSCAQQGC 768

## RESULT 2

ID IL17R\_MOUSE  
 AC Q60943; STANDARD; PRT; 864 AA.  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17 receptor precursor (IL-17 receptor).  
 GN IL17R.

Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=Thymic lymphoma;  
 MEDLINE=96111968; PubMed=8777726;  
 Yeo Z., Fanslow W.C., Seidn M.F., Rousseau A.M., Painter S.L.,  
 Comeau M.R., Cohen J.I., Spriggs M.K.;  
 "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a  
 novel cytokine receptor."  
 Immunity 3:811-821(1995);  
 -1- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
 suggesting that additional components are involved in IL17-induced  
 signalling (By similarity).  
 -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
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EMBL; U31993; AAC53357.1;  
 DR MGD; MGI:107399; IL17r.  
 KW Receptor; Transmembrane; Signal; Glycoprotein.  
 FT SIGNAL 1 31  
 FT CHAIN 32 864  
 FT DOMAIN 32 322 INTERLEUKIN-17 RECEPTOR.  
 FT TRANSMEM 323 343 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 344 864 POTENTIAL.  
 FT DOMAIN 809 814 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 54 54 POLY-GLU.  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 206 206 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 8.0%; Score 306; DB 1; Length 864;  
 Best Local Similarity 22.5%; Pred. No. 1.3e-15;  
 Matches 189; Conservative 129; Mismatches 326; Indels 202; Gaps 42;

QY 5 GWRM-----KAAARPL-----CVANEGVGPASRNSGLNITFKYDNCTTILNPVKR 51  
 DB 17 GWLLLLNLVAPGRASPLRLLDPAPVCAQEGLSCKRVKNSCLDQSWIHPIKMLTSPSPKI 76  
 QY 52 HVTADAQNTISQACHDQAVT-ILWS-PCALGIEFLKGRVILBELKSGROCOO--- 106  
 DB 77 YI-----NLVSSTQHGELVPLVLENTLOTDASILLEGAEISVLQATNERLCYKQF 131  
 QY 107 --LILKDPQLNSFKRTGHSOPFLANKFETDVFVVPFSPKINSENYTPFFTRAC 164  
 DB 132 LSMQLHHRKMRFSF-----SHFVVDQGEVTEVTHLKPPIPDGDPNHSKIIFVDC 185  
 QY 165 D-----LILQPDNLACKPFWKPNLNI-----SOH-----GSDMOV 195  
 DB 186 EDSEKMTTSCVSGSLWDP-NITVETLQTHLRVDFTLWNSTPYVLLSFSDSENHS 244  
 QY 196 SFO-----HAPNFGFRFFLYLKLKHE---GPFKRTCKOEOTTTTSCIL 239  
 DB 245 CFDVVKQIFAPRQEEFORANVTFLSKFEHCCHHVQVQPF-FSSCLND-----CLR 296  
 QY 240 QNVSPGDIILBLDDTNTKVMHVALPV--HSP-WA-GPVRNAVITVPLVITSAP 295  
 DB 297 HAVTVCPVFI-----SMT-----VPRPVADIPLMVYGLITLAI-----LLVGSVYL 341  
 QY 296 FTVYCKKQOEIYSHLDESESSSTYTAALPRERLRPRKVIYISADQKQNNVVOVC 355





QY 321 TTTAAL-----PRELR-----PRKVELCYSKDQGNHN 351  
 DB 289 GMLPLLLSLLVATVWLVAGIYILMWRERIKTSFTTLLPPIKVLVYIPSEICPH-- 346  
 QY 352 VVOCEAYFLQDPCGEVALDLDWEDFSLCHGEGWVOKIHESOFILVVCCKMYVDK 411  
 DB 347 TICITFEFLQNCREVEILEWAKKIAEMGPVQMLATKAKADKAVFLLSNDVSYCG 406  
 QY 412 KNYHGGGSGGKGLFLVAVSAIAEKLRQAKGSSAALSKEFIATYDSCBQVPGIL 471  
 DB 407 TCGSGESSESNQ-DLPLAFNLFCSDLR-----SQHLKTVVYVIREIDTKDDYNAL 460  
 QY 472 DLSTKYRMDNLPQCSHL 490  
 DB 461 SVCPKYLMDATAFAEL 479

## RESULT 4

ID YS02\_CAREL STANDARD; PRT; 718 AA.  
 AC Q10128;

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Hypothetical 81.6 kDa protein F56D1.2 in chromosome II precursor.  
 GN F56D1.2  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Rhabditidae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Chisoe S.; Wilson R.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
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 CC  
 CC EMBL; U99997; AA81100.1;  
 CC Wormpep; F56D1.2; CSD1970.  
 DR Hypothetical protein; Transmembrane; Signal.  
 KW SIGNAL 30 POTENTIAL.  
 FT CHAIN 31 718 HYPOTHETICAL PROTEIN F56D1.2.  
 FT TRANSEM 373 393 POTENTIAL.  
 SQ SEQUENCE 718 AA; 81622 MW; 42B9E056288417AA CRC64;

Query Match 3.38; Score 176.5; DB 1; Length 718;

Best Local Similarity 20.68; Pred. No. 0.065;  
 Matches 89; Conservative. 68; Mismatches 165; Indels 111; Gaps 20;

QY 280 VAITPLVVISAF-----TLTVMCRKKQENIYSHLDEESSESTYALPRELRP 333  
 DB 375 IAVVLLILILVAVTGEGYVARDKVRSEVRNI-----ALTE 413  
 QY 334 RPKVELCYSKDQGNHNVVOCEYAFELQDPCGEVALDLDWEDFSLCHGEGWVOKIHESOFILVVCCKMYVDK 393  
 DB 414 PVKVMIVYAD-DNDLRTDCVKILVENLRNCASCDPVEDLEKLITAEQIVPSRNLVDQISS 472  
 QY 394 SOFTIVVCSKGMKYVPDKNYKHKGGSGGKGLFLVAVSAIAEKLRQAKGSSAALS 453  
 DB 473 LKRFILVSDCAEKILDTAESEHQLVQARPADLPFGMEMI-----IRDATNFPARK 529  
 QY 454 FIATYDSCBQV-----GILDLSTKYRMDNLPQCSHLSDHSLDEGLQPCQVPGIL 510  
 DB 530 YAVVRENIIS--PVPPLNALINLPT-FILPEQFAQLTAFLNHVEH-----TERA 575

QY 511 NYFRSKSGRSLY---VAICNHFIDERPWFKEQFVP-----FHPPLLYREPVLKFP 561  
 DB 576 NYTONISEAQIHEWNLCSARMSFFVRPNWLETWKPKDELAALR---LKQSPVIVPI 632  
 QY 562 DSGLVLDVWCKPGPESDCLAVEAVLGATGADQBSQHGGLDDGEARPALGSA 621  
 DB 633 QT-----EED---RIAKSIKYNVPPQALVSD-----DED 663  
 QY 622 LQPLHTVKAQSPDM--PROSGIVDSVSPSELSPLEMEGLSTQDTTSTSLTESVSSSS 679  
 DB 664 LQD--HASEQNQPIILLPPQCG-----PDSO-----SDSESSESSESSESDNE 706  
 QY 680 GLEEEPPALPSK 692  
 DB 707 G--EDPKTIIVK 716

## RESULT 5

ID IL17S\_MOUSE STANDARD; PRT; 499 AA.  
 AC Q5JIE3; Q5JIE2;

DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor  
 DE homolog 1) (IL-17R1) (IL17Rhl) (IL-17ER).  
 GN IL17B OR EV127.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC MEDLINE-2027323; PubMed-10815801;

RA Tian E.; Sawyer J.R.; Largaespada D.A.; Jenkins N.A.; Copeland N.G.;  
 RA Shaughnessy J.D. Jr.;

\*Evi17 encodes a novel membrane protein with homology to the IL17  
 receptor.\*

RT Oncogene 19:2098-2109(2000).  
 RT FUNCTION: Receptor for the proinflammatory cytokines IL17B and

IL17E. May play a role in controlling the growth and/or  
 differentiation of hematopoietic cells.

CC -1 SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);  
 CC Secreted (isoform 2).

CC -1 ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are  
 CC produced by alternative splicing.

CC -1 TISSUE SPECIFICITY: Liver and testis. Expressed at lower level in  
 CC kidney and lung. Expressed in selected T-cell, B-cell and myeloid  
 CC cell lines.

CC -1 MISCELLANEOUS: EV127 is a common site of retroviral integration in  
 CC BXH2 murine myeloid leukemias, localized near the IL17B gene.

CC Proviral integrations result in increased expression of IL17B on  
 CC the cell surface.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC

CC EMBL; AF208108; AAF86049.1;  
 CC EMBL; AF208109; AAF86050.1;

CC MGD; MGI:1355292; IL17B.

DR Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.  
 KW SIGNAL 1 17 BY SIMILARITY

FT CHAIN 18 499 INTERLEUKIN-17B RECEPTOR.

FT DOMAIN 28 286 EXTRACELLULAR (POTENTIAL).

FT TRANSEM 307 307 POTENTIAL.

FT DOMAIN 308 499 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 67 67 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).





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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL; X75208; CAAS3021.1;  
 DR HSP; P29323; IBAF; 75-06  
 DR Genew; HGNC:3394; EPHB3  
 DR MM; 601839;  
 DR InterPro: IPR001090; Ephrin\_receptor.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003962; FN\_III\_repeat.  
 DR InterPro: IPR001660; SAM.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR InterPro: IPR001426; YKase\_receptor.  
 DR Pfam; PF00041; fn3\_2.  
 DR Pfam; PF00069; pkinase\_1.  
 DR Pfam; PF00536; SAM\_1.  
 DR Pfam; PF01404; EPH\_III.  
 DR PRINTS; PR00014; FN\_III.  
 DR PRINTS; PR00109; TYR\_KINASE.  
 DR PRODOM; PD000001; Euk\_pkinase\_1.  
 DR PRODOM; PD001495; Ephrin\_receptor\_1.  
 DR SMART; SM00060; FN3\_2.  
 DR SMART; SM00454; SAM\_1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP\_1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM\_1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR\_1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1\_1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2\_1.  
 DR PROSITE; PS00105; SAM\_DOMAIN\_1.  
 DR Transferrase; Tyrosine-protein kinase: ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1..33  
 FT CHAIN 34..998  
 FT DOMAIN 34..559  
 FT TRANSHEM 560..580  
 FT DOMAIN 581..998  
 FT DOMAIN 199..336  
 FT DOMAIN 337..448  
 FT DOMAIN 449..544  
 FT DOMAIN 633..896  
 FT DOMAIN 925..989  
 FT SITE 996..998  
 FT NP\_BIND 639..647  
 FT BINDING 665..665  
 FT ACT\_SITE 758..758  
 FT MOD\_RES 608..608  
 FT MOD\_RES 614..614  
 FT MOD\_RES 732..732  
 FT MOD\_RES 942..942  
 FT CARBOHYD 351..351  
 FT CARBOHYD 445..445  
 SQ SEQUENCE 998 AA; 110286 MW; 57C82C397CC61103 CRC64;

Query Match 2.88; Score 109; DB 1; Length 998;  
 Best Local Similarity 18.94; Pred. No. 2.3;  
 Matches 157; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

OY 1 ADTCGWRKAAARPLC-----VANEGVGA-----SRNSG-----LYNIFY 39  
 DB 268 ACTCATGHEPAKESQRCPCPSYKAGGEGCLPCPPNRSIPASICTCHNNFYA 327  
 OY 40 DN-----CTTVLNVKGVIAQNIITISQVACHQDVATILMS-PSALGIEFLKGRV 92  
 DB 338 DSDSADACTVTPSP-PRGVISN-----NETSLIWESEPRDLGVRODLYNV 375

OY 93 ILLEELKSG-----ROCOOLILKDPKOLNSSFKRTGMSQPLNKKPETFYFVKVPPPS 147  
 DB 376 ICKCKGAGGAGSACSDONVEFVROLGLSEPRVTS-----HLARTATTEVOANG 430  
 OY 148 IKWENYIPFFFRACDILLLOPDNLACKFPWPRNLNLSHGSDMOVSDFHAPHFGR 207  
 DB 431 VSKSPLPRTAANNITWQAPSEV-----PTLRHSSSGSLILSHAPPERNG-- 481  
 OY 208 FTLHYKLKAGPP-KKTKCKQQTETTSCLQNVSP-GDYIIELVDDTNTTKVMTA 265  
 DB 482 VLDYEMKY---FEKSEGIASVTTSQMSVQLDGLRDPARYVOV-----RARTVAGT 532  
 OY 266 --LKPVH---SPWAGPIRAVAITVPLVVISAFATL-----FTVNCRRKQENITSH 311  
 DB 533 QYSPAEFTTSSERGSAOQLQOLPLIVGSATAGLVFVAVVIAIVCLKQRH----- 587  
 OY 312 LDESSSESTTAAALPRERLRPRKVFCTYSSKQGNHNNVOCFAVFLQDFC-GCEVAL 370  
 DB 588 -----GSDSEYTEKL-QQYIAPGNKVIIDPTIEDPN--EAVREFAKEIDVSKIEEVI 639  
 OY 371 DLWEDFSLCRECEWYQIKHESQFIIIVCSKGMKVFYDKNKKYHKGSGSGKGLFL 430  
 DB 640 GAGEFGEVCR-----GRKQPGREVF- 561  
 OY 431 VAVSAI---AEKLRAKSSSAALSKEFIAYFYDSRGDVPGLDLS---TKYR----- 478  
 DB 662 VAIKLRKGYTYRQRDFLSEASINGQF-----DHPNITRLGVVYTKSRFVNL 710  
 OY 479 --LMDNLPLQCSHLRSRDLGLOPQOHT-----RQGSERNY-FRSKSGRS 520  
 DB 711 TEFMENC-ALDSFLRLND-----GOFTVQLVGLRLGIAAGKYLSEMTVHRDLAARN 763  
 OY 521 LVY---AIC-----NHOFIDREPDWFEKQFVPPHP-----PLRYREP---VLKSPDS 563  
 DB 764 ILVSNLNVCKYSDGLSRLEDDPS-----DPTTSSLGKIPINWTAPEATATKFTS 817  
 OY 564 -----GLVLDNVCKEPGESDFCLKVAANVAGTGPADSOHESQHGCLDQGEARPAL 616  
 DB 818 ASDVNSYGIWAVEVNS-----TGERPYMNSQDVINAVQDTRLPFPN 861  
 OY 617 DGSAAQLPLHTVAGSPSPDRSDGIYDS-----SVPSSESLIPLMEGLS 662  
 DB 862 DCPALHQLMLDCWVRDRLNRPKFIQVITLKLIRNAASLKVIASAGSGMSPLDRTV 921  
 OY 663 TDQTTSSLTSSVSSSGLEEPEPALPSKLLSGSKADLCGRSYTDEL 712  
 DB 922 PDYTFVTGWLDAIK-MGRYK-----ESFVSAGFASFDLVAQMTAEDL 965

## RESULT 8

PTP6\_DOMO STANDARD; PRT; 1462 AA.  
 AC P16620;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase DTP precursor (EC 3.1.3.48) (Protein-  
 DE tyrosine-phosphate phosphohydrolase).  
 GN PTP69D OR DPTP.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID:7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-90045860; PubMed-2554325;  
 RT "A Streuli M., Krueger N.X., Tsai A.Y.M., Salto H.;  
 RL and Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 CC -!- FUNCTION: IT IS POSSIBLE THAT DTP IS A CELL ADHESION RECEPTOR.

CC CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O -> protein  
 CC CC tyrosine + phosphate.  
 CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC CC  
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 CC CC  
 CC CC EMBL: M27699; AAA28842.1;  
 CC CC PIR: B36182; B36182.  
 CC CC DR HSP: P18052; LYFO.  
 CC CC DR FlyBase: FB00014007; Ptp69D.  
 CC CC DR InterPro: IPR003961; FN.III.  
 CC CC DR InterPro: IPR003806; Ig\_Lc.  
 CC CC DR InterPro: IPR003598; Ig\_C2.  
 CC CC DR InterPro: IPR003600; Ig\_Like.  
 CC CC DR InterPro: IPR00387; Tyr\_Pp.  
 CC CC DR InterPro: IPR00242; Tyr\_PP.  
 CC CC DR Pfam: PF00041; fn3; 3.  
 CC CC DR Pfam: PF00047; Ig; 2.  
 CC CC DR PRINTS: PR00102; Y-phosphatase; 2.  
 CC CC DR PRINTS: PR00700; PTPPHPTASE.  
 CC CC DR SMART: SM00060; FN3; 3.  
 CC CC DR SMART: SM00410; IG\_Like; 1.  
 CC CC DR SMART: SM00408; IGC2; 1.  
 CC CC DR SMART: SM00194; PTPC; 2.  
 CC CC DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 CC CC DR PROSITE: PS00383; TYR\_PHOSPHATASE\_2; 2.  
 CC CC DR PROSITE: PS00356; TYR\_PHOSPHATASE\_PTP; 2.  
 CC CC DR PROSITE: PS00355; TYR\_PHOSPHATASE\_PTP; 2.  
 CC CC KW Hydroxylase; Receptor; Glycoprotein; Signal; Transmembrane;  
 CC CC Cell adhesion; Immunoglobulin domain; Repeat.  
 CC CC FT SIGNAL 1 23  
 CC CC FT CHAIN 24 1462 PROTEIN-TYROSINE PHOSPHATASE DPTP.  
 CC CC FT DOMAIN 24 805 EXTRACELLULAR (POTENTIAL).  
 CC CC FT TRANSMEM 806 823 POTENTIAL.  
 CC CC FT DOMAIN 824 1462 CYTOPLASMIC (POTENTIAL).  
 CC CC FT DOMAIN 38 119 IG-LIKE C2-TYPE DOMAIN 1.  
 CC CC FT DOMAIN 147 221 IG-LIKE C2-TYPE DOMAIN 2.  
 CC CC FT DOMAIN 332 437 FIBRONECTIN TYPE-III 1.  
 CC CC FT DOMAIN 438 538 FIBRONECTIN TYPE-III 2.  
 CC CC FT DOMAIN 912 1165 PROTEIN-TYROSINE PHOSPHATASE 1.  
 CC CC FT DOMAIN 1298 1459 PROTEIN-TYROSINE PHOSPHATASE 2.  
 CC CC FT ACT\_SITE 1097 1097 BY SIMILARITY.  
 CC CC FT ACT\_SITE 1391 1391 BY SIMILARITY.  
 CC CC FT DISULFID 45 112 POTENTIAL.  
 CC CC FT CARBOHYD 40 40 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 58 58 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 64 64 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 85 85 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 105 105 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 109 109 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 119 119 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 162 162 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 191 191 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 196 196 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 209 209 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 255 255 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 288 288 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 302 302 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 429 429 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 442 442 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 451 451 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 516 516 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 613 613 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC CC FT CARBOHYD 701 701 N-LINKED (GLCNAC... ) (POTENTIAL).

FT CARBOHYD 755 755 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 1462 AA; 167411 MW; 8091698930EB CRC64;  
 Query Match: 2.74; Score 104; DB 1; Length 1462;  
 Best Local Similarity: 20.04; Pred. No. 9.3;  
 Matches: 88; Conservative: 53; Mismatches: 136; Indels: 164; Gaps: 23;  
 QY 20 NEGVGASR-----NSGLNITFKYD-----NCTYLNPGKHEVIADA 57  
 DB 259 NDGNDFQFFITLQEAQPTFTYHDFKNGSHSYILDHFKPNTTYFLRVKNSING 318  
 QY 58 -----QNTISQYACHDOV-----AVTILSGALG-IPLKGFVILEEL 97  
 DB 319 OPTQYPOGIIITLSY---DPFIKPVETGTASTITIGMPPPPDLIDYIQLYELVSE- 374  
 QY 98 KSGRQCQQLIKADKPOLNSPRTGHSQPELAKMKPTDYFKVVPFSSIKNSNTHPF 157  
 DB 375 --86-----EVKVEEATCOOSRNLPTN-----FUKLATDYE-- 408  
 QY 158 FFRTRACDILLQPMACKPPW-----KPRKUNISQH-----GSDMQVSF 197  
 DB 409 -FVRACSDLTG---TCGP-WSENVNGTMDGVATKPTNLSIOCHHDNVTGNSIAINW 462  
 QY 198 DHAPHNFGFRFTYL-----HYLKRHE--GPKFKATC--- 226  
 DB 463 DVPKTPNGKWSYTLHLGNPMSTVDREMGPKIRRIDEPHRTKLTYESVSPNTNTVTVS 522  
 QY 227 -----KQEQTTTSCLLONVSGDYIELVDVNTYTKVNHVALK---PVHSPWAGPIR 278  
 DB 523 AITREKNGEPATGSLAPYSTPDAGRTWMSKVNLSK---YVLKLYLPKISBNGPI- 578  
 QY 279 AVAITPLVVISAFATLETWCKKQOE-----NIYSHLDES---SESSTYALPR 328  
 DB 579 -----CCRYLVRINDNRELDPPEKLNATYQVEHSNDVTRSSAYIAEMIS 626  
 QY 329 ERLRPKPVLCYSSKQGNH 349  
 DB 627 SKYF-RPEIFLGAERFSENN 646

## RESULT 9

RGFP2\_HUMAN STANDARD; PRT; 663 AA.  
 ID RGFP2\_HUMAN  
 AC P47736;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rapi GTPase activating protein 1 (RapiGAP).  
 GN RAPIGAP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-91256304; PubMed-1904317;  
 RA Rubinfeld B., Mumentals S., Clark R., Conroy L., Watt K.,  
 RA Crozier W.J., McCormick F., Polakis P.,  
 RT Molecular cloning of a GTPase activating protein specific for the  
 RT Krev-1 protein p21rac1.  
 RL Cell 65:1033-1042(1991).  
 RN [2]  
 RP TISSUE SPECIFICITY, AND INDUCTION.  
 RX MEDLINE-98010656; PubMed-9346962;  
 RA Kurachi H., Wada Y., Tsukamoto N., Maeda M., Kubota H., Battori M.,  
 RA Iwai K., Minato N.;  
 RT Human SPA-1 product selectively expressed in lymphoid tissues is a  
 RT specific GTPase-activating protein for Rapi and Rap2.  
 RL J. Biol. Chem. 272:28081-28088(1997).  
 CC -1- FUNCTION: GTPase activator for the nuclear res-related regulatory  
 CC protein Rap-1a (KREV-1), converting it to the putatively inactive  
 CC GDP-bound state.

CC -1- SUBCELLULAR LOCATION: Associated with Golgi membranes.  
 CC -1- TISSUE SPECIFICITY: Significant expression seen in the brain,  
 CC kidney and pancreas. Abundant in the cerebral cortex and expressed  
 CC at much lower levels in the spinal cord. Not detected in the  
 CC lymphoid tissues.  
 CC -1- INDUCTION: By 12-O-tetradecanoylphorbol-13-acetate (TPA) in  
 CC promyelocytic HL-60 cells.  
 CC -1- SIMILARITY: CONTAINS 1 RAP/RAN-GAP DOMAIN.

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CC EMBL; M64788; AAA60252.1;  
 CC GenBank; U01147; AAC50063.1;  
 CC MIM; 600276;  
 CC InterPro; IPR003109; GTPase\_IGN.  
 CC InterPro; IPR000331; Rap\_GAP.  
 CC Pfam; PF02145; Rap\_GAP; 1.  
 CC Pfam; PF02188; GoLoco; 1.  
 CC SMART; SM00390; GoLoco; 1.  
 CC GTPase activation; Membrane.  
 CC FT DOMAIN 210 397  
 CC RAP/RAN-GAP.  
 CC SEQUENCE 663 AA; 73391 MW; 3703B7CC603404DA CRC64;

Query Match 2.74; Score 103.5; DB 1; Length 663;  
 Best Local Similarity 19.58; Pred. No. 3.4;  
 Matches 143; Conservative 80; Mismatches 262; Indels 247; Gaps 33;

QY 132 MKETFDYFVKVVPSPKESNTHVFFTRACDLLOPD-----171  
 DB 21 LATEEDY----IPYFSV-----EVLGREGFPPLILLPQFGYEGTNHETISIPETE 70  
 QY 172 -----NLAKP-----FWKPRMLNISQSDMQVSDHAPHNFGPRFFLYHYK 214  
 DB 71 PQSPPTTKVLEKENTARIYKFKLKEHFN-----YSLDTA-----LGLHVFSLKYD 119  
 QY 215 L-----KHGPFKKTKCKQEQTTETSCLLQNVSPGDYIIELVDDVTNTRKVMHVALKPVH 270  
 DB 120 VIGDQELRLRLTRCTRYEDVPIPCSLTEFFENVVQAKLVCEVDNVDR-----FYPVL 173  
 QY 271 SPWAGPIRAVAITVPLVVIS---AFATLFTVMCRKQKQENIYSHLDEESSESYTTAALP 327  
 DB 174 YPKAS---RLIVTFDEHVISNFKFGVIYKLGQTSEE-----LSTNEESPAPVEFL 225  
 QY 328 RRLRLPRKVFELCYSSKQDQNMNVQCFAYELQDQCCCEVALDLWE-----DFSLCR-- 360  
 DB 226 -----FLQKVK-----LQDFKGRGLDVTGHTGTSYCNFR 260  
 QY 361 -----EGREWVOKTHESQFIIVVCSGMKMYFDK-----NRYK 415  
 DB 261 NKEIMFHVSTKLYTGESDAQOLQRKHGNDIVV-----VFQDENTFFVPMIANSFL 314  
 QY 416 H-----KGGGRSGRGELFVAVSAIAE-----KLKQKQSSAALSFKFIA 456  
 DB 315 HAYVVOAEGGG---PDGLPKVSVTARDVDFPGPLPDPAVERKGPQFQLTLKLIN 371  
 QY 457 VFDYSC-EGDVPFGILOLSTKYRLMDNLPOLCSHLHSD-HGLQEPQHTGTRGRNYF- 513  
 DB 372 A--EYACYAKFAKFALETRALLETLYEEL-HHSQSMGLGDEGCKMENGSGGGFF 428  
 QY 514 -----RSKSGSL-----YVACNHEQPIDEEDWFE-----KQFVFPFPLPLR 552  
 DB 429 ESFKVIRSRSGSDMAGLSNKNKNTVTSHSGSPAPNPDAAKAGISLVIPKSGSPTRK 488  
 QY 553 YREPVLEKFDGLVNDVNYCKPGPESDFCLKVAAYAVLGATGSPADQSQHSQGGGLDQGEA 612  
 DB 489 KSGPFGSRSSAIGIENT-----QEVQEKRESPPAGKTP-DSGHVSEQPKSE----- 535

QY 613 RPAIGSAAALQPLRTVTKAGSPDMPDSGTYSSVSELS-----LPLMEGLSTDQTE 667  
 DB 536 ---NSTQSPFPTTKNRTAQAARALKDFSSSSASSASVSVETEGVGDGNG 591  
 QY 668 TSS-----LTSYSSSSG-----LGEEDPALPSKL 693  
 DB 592 LRSVSSSGTPHKRDSFYITWLEDSVSTTGGSPGSPSRPHDAGKLGDPACPEIKQL 651  
 QY 694 LSGSGCKADLQC 705  
 DB 652 EASEQMPQLQC 663

RESULT 10  
 ABR\_EDMAN STANDARD: PRT; 859 AA.  
 AC Q12979: Q13693: Q13694;  
 DT 15-JUL-1999 (Rel. 38: Created)  
 DT 15-JUL-1999 (Rel. 38: Last sequence update)  
 DT 13-JUN-2002 (Rel. 41: Last annotation update)  
 DE Active-breakpoint cluster region-related proteola.  
 GN ABR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Bioprocampus.  
 RX MEDLINE=94086546; PubMed=8262969;  
 RA Tan E.-C., Leung T., Manser E., Lim L.;  
 RT "The human active breakpoint cluster region-related gene encodes a  
 RT brain protein with homology to guanine nucleotide exchange proteins  
 RT and GTPase-activating proteins."  
 RL J. Biol. Chem. 268:27291-27298(1993).  
 RN [2]  
 RP SEQUENCE OF 39-859 FROM N.A. (LONG AND SHORT FORMS).  
 RC TISSUE-Fibroblast;  
 RX MEDLINE=93352463; PubMed=849582;  
 RA Helsterkamp N., Kaartinen V., van Soest S., Bokoch G.M., Groffen J.;  
 RT "Human ABR encodes a protein with GAPrac activity and homology to the  
 RT DBL nucleotide exchange factor domain."  
 RL J. Biol. Chem. 268:16903-16906(1993).  
 RN [3]  
 RP SEQUENCE OF 436-597 FROM N.A.  
 RX MEDLINE=90067847; PubMed=2587217;  
 RA Helsterkamp N., Morris C., Groffen J.;  
 RT "ABR, an active BCR-related gene."  
 RL Nucleic Acids Res. 17:8821-8831(1989).

CC -1- FUNCTION: GTPASE-ACTIVATING PROTEIN FOR RAC AND CDC42. PROMOTES  
 CC THE EXCHANGE OF RAC OR CDC42-BOUND GDP BY GTP, THEREBY ACTIVATING  
 CC THEM.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: HIGHLY ENRICHED IN THE BRAIN. MUCH WEAKER  
 CC EXPRESSION IN HEART, LONG-AND MUSCLE.  
 CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.  
 CC -1- SIMILARITY: STRONG, TO HUMAN BCR.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL; U01147; AAC50063.1;  
 CC EMBL; L19704; AAC37519.1;  
 CC EMBL; L19705; AAC37518.1; ALT\_INIT.



Query Match 2.69; Score 101; DB 1; Length 1275;  
 Best Local Similarity 19.29; Pred. No. 13;  
 Matches: 98; Conservative: 66; Mismatches: 144; Indels: 202; Gaps: 24;

QY 91 RVILEELKSGRCOOL-ILAD-----PKOLNSPFTGME-----SOPFLAKMFFEDTVK 141  
 DB 243 QVFSMLEAEVQVQHLVWFLPLMASSKRPYTHDDVSIFLNS--ETIFLH 300  
 QY 142 VYFSPSTKNSNTHFFTRACDLILQDNLACKPFWKPNLNSQ-----HGSMDQVS 196  
 DB 301 QIFYOGLKARISWPTLVIALDLILLP-----MLNIYDFVRNHOYSLOI- 346  
 QY 197 FDHAPHNFGFRPFLYHLYKHGSPFKATCKOBTETTSCLLQNVSPGDIYILVD-- 253  
 DB 347 LAHQKQNRDFDKLKHAEKPD-----C-EERTLETFYIPAFQIP-RYILTLADVLA 397  
 QY 254 ---DINTTRAVMHAIAKPVHSPWAPIRAVAITVPLVISAFAATLFTVWCKQOENIS 310  
 DB 398 HTPHEHVERNSLOXA-----KSKLELSR 421  
 QY 311 HLDSESESYTAALPRLPRPRLPVFLCYSSKQONHNVVQCFAYFLQDFGCEVAL 370  
 DB 422 INHDEVESEINIKLALERA-----IIE-----GCEILL 451  
 QY 371 DLWEDF-----SLCRGORENVKTHESQFTIVVCSKGM 405  
 DB 452 DTSQTFVROGSLQVPMSEKQITRGLGSLSLKEGEGOCFLFSKH-----LIICRGS 506  
 QY 406 --RYFVDKKN-----KHGGG-----RGSGKGLFLVA 432  
 DB 507 GGLHLTKNGVISLIDTLLEPEESTEEAKSGQDIDHLDKFIKVPKDSPPFTVILVA 566  
 QY 433 VSAIAELKRAQKSSAALSFFIATYDYSCEGDFGILDLSTKYRLMDNLPLQCLSHLS 492  
 DB 567 SS-----ROKAAWTSLSQCVQD-----NIRCMANNAFENSKV-----TVPMI- 608  
 QY 493 RDRGLQBPQGTROGSRNRYFRSKGRSLY 522  
 DB 609 -----KRTGCTRAEN-SRSDASLY 628

RESULT 12  
 Z151\_MOUSE STANDARD; PRT; 794 AA.  
 AC Q60821; 060699;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Zinc finger protein 151 (Polymavirus late initiator promoter binding  
 DE protein) (LP-1) (Zinc finger protein z13).  
 GN ZNF151 OR ZFP100.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid-10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Rapp L., Carmichael G.G.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CBA; TISSUE-Kidney;  
 RX MEDLINE-96003919; PubMed-7575457;  
 RA Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;  
 RT "An unusual arrangement of 13 zinc fingers in the vertebrate gene  
 RT z13".  
 RL Biochem. J. 311:219-224(1995).  
 CC 1- FUNCTION: MAY FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT  
 CC REGULATES THE EXPRESSION OF SPECIFIC GENES.  
 CC 1- SUBCELLULAR LOCATION: Nuclear (potential).  
 CC 1- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES  
 CC EXAMINED.  
 CC 1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-

FINGER PROTEINS.  
 1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.  
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EMBL; U22396; AAA64848.1;  
 EMBL; U14556; AAA85493.1;  
 RSP; P08046; IAIH.  
 MGD; MGI:107410; Zfp100.  
 DR InterPro: IPR000210; BTB\_POZ.  
 DR InterPro: IPR000822; Znf\_C2H2.  
 Pfam; PF00096; zf-C2H2; 13.  
 Pfam; PF06551; BTB; 1.  
 PRINTS; PR00048; ZINC\_FINGER.  
 PRODOM; PD000003; Znf\_C2H2; 1.  
 SMART; SM00355; Znf\_C2H2; 13.  
 PROSITE; PS00097; BTB; 1.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 13.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 13.  
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT DOMAIN 1 104  
 FT ZINC\_FINGER.  
 FT ZINC\_FINGER.  
 FT ZNF\_FING 297 730  
 FT ZNF\_FING 319  
 FT ZNF\_FING 325 347  
 FT ZNF\_FING 353 375  
 FT ZNF\_FING 381 403  
 FT ZNF\_FING 409 431  
 FT ZNF\_FING 437 459  
 FT ZNF\_FING 465 487  
 FT ZNF\_FING 493 515  
 FT ZNF\_FING 519 543  
 FT ZNF\_FING 549 571  
 FT ZNF\_FING 577 599  
 FT ZNF\_FING 605 628  
 FT ZNF\_FING 708 730  
 FT ZNF\_FING 708 730  
 FT CONFLICT 507 507  
 FT CONFLICT 573 573  
 SQ SEQUENCE 794 AA; 86664 MW; FFF8856DEBF7ED CRC64;

Query Match 2.69; Score 99.5; DB 1; Length 794;  
 Best Local Similarity 20.69; Pred. No. 8.9;  
 Matches: 71; Conservative: 41; Mismatches: 146; Indels: 87; Gaps: 15;

QY 364 CGCEVALDLWEDSLCRGORENVKTHESQFTIVVCSKGM-KYFDKKNYKHGGRG 422  
 DB 24 CDCTFFVD-GVDF-----KAHKA-VLAACEYFALFVQKQVVDVILDSNA 67  
 QY 423 SGKGLFLVAVSAIAELKRAKQSSS-----AALSFIATYFYSCEGDFGILDLST 475  
 DB 68 AGLGQ-----VLEFMYTAKLSLPENVDDVLAVASFLQMO-----DIVT 106  
 QY 476 KYRLMDNLPLQCLSHL-HSRDRGLQEPQH-----TROGSRNRYFRSKGRSLY 522  
 DB 107 ACHTLKSLAEPSTTGESADASAEGGDKRAKAAATMLSLQAGSSSTSGRELK 166  
 QY 523 VAICNMHQFIDEEDPWEKQFVFPHPPLRYREPVLEKFDGLVLDNVMYKPGPESDFCL 582  
 DB 167 EERGGQAESASSGARQTEKADAPREPP-----VELKPDPTSSMA- 206  
 QY 583 KYEAVVIGATGPAUSQSHESQHGGLDQDGEARPDGSAALPLIHTVYKAGSPSPDRSG 642  
 DB 207 AAALALSSSSQMEVEPKAG--EDGQEEGAGPATVKEGHH-LONGEPPEEESA 263  
 QY 643 IYDSSYPSSLSLP---LMRGLSTQDTSTSLTSSVSSSGLEE 684

DB 264 GTDS---GQELHGEONLSGTIGRTESKAYGSIHRCDCGKE 305

## RESULT 13

2F72\_MOUSE STANDARD/ PRT; 783 AA.

AC P206621

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Zinc finger Y-chromosomal protein 2

GN ZFY2 OR ZFY-2

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89168416; PubMed=2493989;

RA Mardon G., Page D.C.,

RT "The sex-determining region of the mouse Y chromosome encodes a

protein with a highly acidic domain and 13 zinc fingers."

RL Cell 56:765-770(1989).

CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-

FINGER PROTEINS. ZFY/ZFY SUBFAMILY.

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or send an email to [license@sib.ch](mailto:license@sib.ch)).

CC EMBL, M24401; AAN56845.1;

DR FIR; A31491; A31491.

DR HSP; P08048; ZNF.

DR MGD; MGI:99213; Zfy2.

DR InterPro; IPR000822; Znf\_C2H2.

DR Pfam; PF00096; zf-C2H2; 13.

DR PRINTS; PR000048; ZINCFINGER.

DR ProDom; PD000003; Znf\_C2H2; 1.

DR SMART; SM00355; Znf\_C2H2; 13.

DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 7.

DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 10.

KW Transcription regulation; Activator; Zinc-finger; Metal-binding;

KW DNA-binding; Repeat; Nuclear protein

FT DOMAIN 372 382 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 403 777 ZINC FINGERS.

FT ZN\_FING 403 425 C2H2-TYPE.

FT ZN\_FING 434 456 C2H2-TYPE.

FT ZN\_FING 466 488 C2H2-TYPE.

FT ZN\_FING 497 520 C2H2-TYPE.

FT ZN\_FING 526 548 C2H2-TYPE.

FT ZN\_FING 554 577 C2H2-TYPE.

FT ZN\_FING 583 605 C2H2-TYPE.

FT ZN\_FING 611 634 C2H2-TYPE.

FT ZN\_FING 640 662 C2H2-TYPE.

FT ZN\_FING 668 691 C2H2-TYPE.

FT ZN\_FING 697 719 C2H2-TYPE.

FT ZN\_FING 725 748 C2H2-TYPE.

FT ZN\_FING 754 777 C2H2-TYPE.

SQ SEQUENCE 783 AA; 88856 MW; 1722D1C23F019D88 CRC64;

Query: Match

Best Local Similarity 19.23; Score 99; DB 1; Length 783;

Matches 117; Conservative 74; Mismatches 207; Indels 210; Gaps 34;

OY 36 TFKDNCVTTLNPGKHVHTADQNTISQYACHDQVAVVILWSPGALGTEFLKGRVILE 95

DB 339 TAAINDNSDEI-----EVQNTATASAMLRHDESG-----GLD-----RVPKQ 374

OY 96 ELAS---EGRCOOLILADPKQLNSGFRTGMSQP---FLANKPFTDYFVYVPPPSIK 149  
DB 375 KSKKKRPESKQTSALVADQQT-----LRYTPMGCGKFKFKFLA---RHIA 423  
OY 150 NESNYHFFFRTRACDLLODLNACKPFWKPNLNISQSGDMQVSPDPAHFGFRFF 209  
DB 424 N-----HPEYLANKY---HCTEDYSTNKKIS----- 448  
OY 210 YLHYKLKGGPPKRTCKQEQYTTTSCLLQNVSPGYIITELVDVDTNTRKVMYALKPV 269  
DB 449 -LNNHESH---KLTIKTEKTCDDC-RKNLSHA-----GTLCTHKTMTTE--- 490  
OY 270 HSPWAGPIRAVAITVPLVVI---SAFATLFT---VMCRKQCOENIYSHLDESSESSTY 322  
DB 491 -----RGVNKTCCKCFDYETABQTLNHLHVAVERKK---PPIHCGCKGKGRH 537  
OY 323 TALLPRE-ELRPRPVFLC---YSSKQGN---HMYVQCFAVFLDQFCGEVALDWE 374  
DB 538 PSALKHRIHVHIGERTCEYCEKSDSSNLKTHIKSKSKEIPLK---CDICL---L 590  
OY 375 DFSLCRGGREWVI---OKTHESQIIVVCSKGMKVFVDKNNYKHGGGSGGKGLFLV 431  
DB 591 TFSYTKAQOCHAVLHQSERTHQ---CS-----HCNHSKSSNSDLARHISV 633  
OY 432 AVSAIAEKLRQAKQS---SSAALSKFIAVTFDYS---CEGDPVPG-----IDLSTK 476  
DB 634 HTRAYPHKCDMC-SKGFHRPSLAKKRVATEKSKMKHOCNCDPNSDPPLLSHLSAHTK 693  
OY 477 YRLMDNLPLC-SHLSRDLGLOEPOGTRGSRNTRPSKSGSLVAICNKHOFIDEEP 536  
DB 694 -----NVPEKCRCKK-----EPQOOCLOTHNTHSSRVYQ---CEYCSYSDA 737  
OY 537 DWPEKQVFPHPPPPIRYREPVLKESGLVLDVWCKPESDFPKLVEAVLGTATPAD 596  
DB 738 SGKRRVVISLHTNDYPHR-----CDFCKK-----GFRPSE 768  
OY 597 -SQHESQH 603  
DB 769 KNOHIMRH 776

## RESULT 14

PSU1\_YEAST STANDARD; PRT; 970 AA.

AC P53550;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE mRNA decapping protein 2 (PSU1 protein).

GN DCP2 OR PSU1 OR INL118C OR NI917.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=D273-10B;

RL Tzagoloff A.A.;

RN [2]

RP Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97245296; PubMed=9090055;

RA De Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,

RA Pallavicini A., Lanfranchi G., Valle G.;

RT "The DNA sequence of cosmid 14-13b from chromosome XIV of

Saccharomyces cerevisiae reveals an unusually high number of

overlapping open reading frames."

RL Yeast 13:261-266(1997).

RN [3]

RP INTERACTION WITH DCP1.

RX MEDLINE=99438017; PubMed=10508173;

RA Duckley T., Parker R.;



RT "The DCP2 protein is required for mRNA decapping in Saccharomyces cerevisiae and contains a functional 'nutr motif'."

BL EXB0.7 18.5(11-5422(1999)).

CC -1- FUNCTION: REQUIRED FOR THE PRODUCTION OF ACTIVE DECAPPING ENZYME, PHENANES IN A PROCESS REQUIRING THE HYDROLYSIS OF A PYROPHOSPHATE BOND. DECAPPING IS A THE MAJOR PATHWAY OF MRNA DEGRADATION IN YEAST. IT OCCURS THROUGH DEADENYLATION, DECAPPING AND SUBSEQUENT 5' TO 3' EXONUCLEOTIC DECAY OF THE TRANSCRIPT BODY.

CC -1- SUBUNIT: INTERACTS WITH DCP1.

CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. STRONG, TO S. POMBE SPAC19A8.12.

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CC EXBL; I43065; AAA68866.1;

DR EXBL; 569382; CAA93389.1;

DR EXBL; 271394; CAA93998.1;

DR SDD; 80005062; DCP2.

DR InterPro; IPR000086; NUDIX\_hydrolase.

DR Pfam; PF00293; NUDIX.1.

DR PRINTS; PR00502; NUDIXFAMILY.

DR PROSITE; PS00893; NUDIX.1.

KW Hydrolase.

FT DOMAIN 134 155 NUDIX BOX.

FT DOMAIN 436 439 POLY-SER.

FT CONFLICT 425 425 P -> L (IN REF. 1).

SQ SEQUENCE 970 AA; 108667 MW; D53CA2C5A546FAAA CRC64;

Query Match 2.6%; Score 99; DB 1; Length 970;

Best Local Similarity 17.9%; Pred. No. 13;

Matches 106; Conservativity 86; Mismatches 182; Indels 218; Gaps 26;

QY 239 LQNVSGDYIE--LV-----DDNTYKVMYALKPVHSP--AGPIRAVAITVP 285

DB 9 LEWTSVRILEDLVFIINCNDLSVERELFEE--EASWFTDFIKLANPTLP 64

QY 286 LVVISAFTLVTCRKQKQNTYSHLDSESSSYTAALP-----RELR----- 332

DB 65 SLAKESFALLIKLCPVWKWDI--RVDEALQOFKYKKSIPVGAATFNENSKILMYQ 122

QY 333 -----PPKPVFLCYSKDCQNMVNVQCFAYFLQFCGCEVALDLWEDFSLCREQ 383

DB 123 GTESDSNSPPREKI--SKD-----ENDIDCCIREVKE--EIGFDLTD----- 160

QY 384 RENVIOKTHESQFIIVCVSGKMYFVDKKNYKHGGSGRGELFLVA--VSAI----- 436

DB 161 -----YIDNQFI-----ERNLOQNTK-----IFLISGVSEVFNPKQ 194

QY 437 -----AEKLR--QAKQSSAALSKFIATFDYS-----CEGD 466

DB 195 VRNEIDKIDNDFKIKSTKYNKYLINSMMRPLSMWRHORIKNEQDOLSKVAEQ 254

QY 467 VPGILDSTKRLMDNLPLQCSLHLSR-----DHGLQEPGQHTR 505

DB 255 LKLLGLI--TKEQIDPGRELLNMLHTAVQANSNNVNSQVPSQEQHLKQSGEHQ 313

QY 506 QGSRNRYFRSGSLVATCN-----MHQFIDEEPWFEE--KQVPE- 546

DB 314 OKQOSSFSQQQSIPPSLSEPPANNKRVIPPTPMANVNSNQLFATNGQPPAPFP 373

QY 547 -----HPPPLRYREPVLKFDGSLVLDVNCVKPGPESDFC 581

DB 374 FMLPLTNNSANPTPTVPPNPNPMPNMAFGVPPNMINLSGPVSPQFSLPPAPL----- 429

QY 582 LKVEAAVLGATGPAADSQHSGG--LDQGEARPALDGSAAQLPQLLTHTVKGSPSMPFR 639

DB 430 -----PRDSYSSSPGQLLDILNSKKPDSNVQSSKKPLKILQRTGLNSIK 477

QY 640 DSGIYDSVPSSELSPLMGLSTDC-----TETSSLTESVSSSGIGEEZ 605

DB 478 QNNDETAHNSQALDLKRTSSQKHASRPTDTSFLPN--DSVSGIQARE 527

RESULT 15

EX3B\_CHELN STANDARD; PRT; 1050 AA.

ID EX3B\_CHELN

AC Q927G7; Q9J5S1; O9K2F2;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Exodeoxyribonuclease V beta chain (EC 3.1.11.5).

GN RECB OR CPN0738 OR CP0007.

OS Chlamydia pneumoniae (Chlamydophila pneumoniae).

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.

OX NCBI TaxID=83558;

RA [1]

RA SEQUENCE FROM N.A.

RC STRAIN=CHL038.

EX MEDLINE=99206606; PubMed=10192388;

RA Kallman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,

RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.,

RA "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."

RL Nat. Genet. 21:385-389(1999).

RN [2]

RN SEQUENCE FROM N.A.

RP STRAIN=AR39;

RC MEDLINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

RA White O., Hickey E.K., Peterson J., Utterback T., Barry K., Bass S.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

RA Gwinn M., Nelson W., DeBoy-R., Kolonay J., McClarty G., Salzberg S.L.,

RA Eisen J., Fraser C.M.,

RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39";

RT Nucleic Acids Res. 28:1397-1406(2000).

RL [3]

RL SEQUENCE FROM N.A.

RC STRAIN=J138;

EX MEDLINE=20330349; PubMed=10871362;

RA Shirai T., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,

RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;

RA "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA";

RT Nucleic Acids Res. 28:2311-2314(2000).

CC -1- FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.

CC ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'- or 3'- to 5'-direction to yield 5'-phosphooligonucleotides.

CC -1- SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.

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CC EXBL; AE001635; AAD18877.1;

DR EXBL; AE002164; AAF37903.1;

DR EXBL; AP002547; BAA98945.1;

DR HSSP; P09980; IUAA.

DR TIGR; CP0007;

DR InterPro; IPR000212; UVRD-helicase.



DR Pfam: PF00580; UvrD-helicase; 1.  
KW Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;  
KW DNA repair; Complete proteome.  
FT NP\_BIND 21 28 ATP (POTENTIAL).  
FT CONFLICT 142 142 N -> K (IN REF. 2).  
FT CONFLICT 182 182 V -> I (IN REF. 1).  
SQ SEQUENCE 1050 AA: 121056 MW: 622003032AE8387 CRC64;

Query Match 2.6%; Score 98.5; DB 1; Length 1050;  
Best Local Similarity 20.4%; Pred. No. 16;  
Matches 120; Conservative 85; Mismatches 201; Indels 181; Gaps 31;  
QY 94 LEEELSESG-----RQCQQLIKQPKQLNLSFKTCHESQPELNKKFETDYFKVVP 144  
DB 348 LEKLLSSSEAPVQALRQYGLVLIDEFQ-DYDKQOWPFSNLFISPKFTGSLFLGDP 406  
QY 145 FPSIKESNYHPPFFTRACDILLQDMLACK----- 176  
DB 407 KOSI-----YERSGADL---PYLTAKSFSEDQQLQLVNVRSTPKLMEALNQI 453  
QY 177 -----PFNK-PRNLISQSGDMQVS--FDHAPNFGFRFFYLHYLKLHSGPKFKTKCQ 228  
DB 454 FGRISPFLEIFGLPIEYHALNPQSSETFENPPHPIHFFYETIKDQALWIFSEALRQ 513  
QY 229 EOTTETTSCLQNVSPDYIIELVDVNTKVMYALAPV-----ESPWA 274  
DB 514 KE-----QKIPLGNVV-LVSDSNQAPELISATIPVSFSKNSIPELTHILTT 563  
QY 275 GPIRAVAITVPLVVIS--AFATLTV---MCKKIQENIY-----SHLDEESSESSTYT 323  
DB 564 ALLEAILHPENYEKISLIFSLFGLSLDEVTYTKEDFTIYFQSLHSTISHGLLATYTR 623  
QY 324 A-----ALPERLRPRPKVFLCYSSKDGQGNHNVQCFAY-----FLDFCGCEVAL 370  
DB 624 VMTQGNVLFSSPBGDLIFQMEKLC-----GYLDTISSYPYHQLHLKNS-----ET 672  
QY 371 DLWED---FSLCRGOREWVIOKHESQFIIVVCSKGMRYFV-----DKNRYHKGGR- 421  
DB 673 GRWEEELAISSYSDLETLKTTIHS-----SKLEYDIVFCPGIEKSKNSSEL 724  
QY 422 -----GSGKGLFVAVSAIAEKLQAKQSSAALSKEIATVFDYSCGDVPGILD 473  
DB 725 LREMTVACTRAKQLYL-PISTOPPSLQR-----SSALNTVYL-----ESTQSSAYDL 772  
QY 474 STKYRLMDNLPOLCSHLHSDHG-----LQEPQHT---RQSSRNRYFRSKGRSLYAI 525  
DB 773 A--IHLQEHDPFSLPDKDGHATVVLNPLLETFAKVTTPPTIFSFSSSTKFL----- 826  
QY 526 CMMQOFIDEEPDPFERQFPPHPPPLRYE-PVLERKFDGLVNDVM 571  
DB 827 -----LQTHKD---SQSIPYKLPISKQQLPLGER--TGILIHKIL 862

Search completed: May 19, 2003, 09:20:55  
Job time : 21.5787 secs

1. The first part of the document is a letter from the President of the United States to the Congress, dated January 3, 1862. It is a very important document, as it contains the President's annual message to Congress. The letter is written in a very formal and dignified style, and it is one of the most important documents in the history of the United States.

2. The second part of the document is a report from the Secretary of the Treasury, dated January 3, 1862. It is a very important document, as it contains the Secretary's report on the state of the Treasury. The report is written in a very formal and dignified style, and it is one of the most important documents in the history of the United States.

3. The third part of the document is a report from the Secretary of the Interior, dated January 3, 1862. It is a very important document, as it contains the Secretary's report on the state of the Interior. The report is written in a very formal and dignified style, and it is one of the most important documents in the history of the United States.

4. The fourth part of the document is a report from the Secretary of the War, dated January 3, 1862. It is a very important document, as it contains the Secretary's report on the state of the War. The report is written in a very formal and dignified style, and it is one of the most important documents in the history of the United States.

5. The fifth part of the document is a report from the Secretary of the Navy, dated January 3, 1862. It is a very important document, as it contains the Secretary's report on the state of the Navy. The report is written in a very formal and dignified style, and it is one of the most important documents in the history of the United States.

GenCore version 5.1.4 ps\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:14:29 ; Search time 56.3267 seconds  
(without alignments)  
2636.495 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_36\_753  
Perfect score: 3829  
Sequence: 1 AUCGWRKAAARPLCVAN.....CGLDGRSYDELHVAFL 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 04

Maximum Match 100%  
Listing first 45 summaries

Database:

SPRMBL\_21.\*  
1: sp.archaea.\*  
2: sp.bacteria.\*  
3: sp.fungi.\*  
4: sp.human.\*  
5: sp.invertebrate.\*  
6: sp.mammal.\*  
7: sp.mhc.\*  
8: sp.organelle.\*  
9: sp.phage.\*  
10: sp.plant.\*  
11: sp.rodent.\*  
12: sp.virus.\*  
13: sp.vertibrate.\*  
14: sp.unclassified.\*  
15: sp.virus.\*  
16: sp.bacteriap.\*  
17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3005	78.5	564	Q9UFA0	Q9UFA0 homo sapien
2	2616.5	68.3	582	Q8E5J8	Q8E5J8 mus musculus
3	1950.5	50.9	745	Q8QJ39	Q8QJ39 brachydactyl
4	1941.5	50.7	745	Q8QJ39	Q8QJ39 brachydactyl
5	170.5	4.5	846	Q9NA84	Q9NA84 caenorhabditis
6	117.5	3.1	562	Q99755	Q99755 homo sapien
7	117	3.1	757	Q13399	Q13399 ustilago ma
8	116.5	3.0	901	Q9KE04	Q9KE04 bacillus ha
9	112.5	2.9	549	Q99754	Q99754 homo sapien
10	111.5	2.9	348	Q9H460	Q9H460 homo sapien
11	111.5	2.9	370	Q96KN9	Q96KN9 homo sapien
12	110	2.9	428	Q9NTU6	Q9NTU6 homo sapien
13	110	2.9	917	Q81789	Q81789 arabidopsis
14	108	2.8	903	Q95W47	Q95W47 bulla gould
15	108	2.8	1058	Q9AY10	Q9AY10 oryza sativ
16	108	2.8	1962	Q9WUF3	Q9WUF3 mus musculus

17	107.5	2.8	938	11	Q60669	Q60669 mus musculus
18	107.5	2.8	3788	11	Q922X9	Q922X9 rattus norv
19	107.5	2.8	3942	11	Q88737	Q88737 mus musculus
20	107	2.8	1322	11	Q9QZP6	Q9QZP6 mus musculus
21	106.5	2.8	638	10	Q9LQF8	Q9LQF8 arabidopsis
22	106.5	2.8	1907	4	Q15017	Q15017 homo sapien
23	106	2.8	593	11	Q99PV2	Q99PV2 rattus norv
24	106	2.8	1516	4	Q9C0D2	Q9C0D2 homo sapien
25	106	2.8	1545	11	Q9V8S6	Q9V8S6 mus musculus
26	106	2.8	3788	11	Q9P7412	Q9P7412 mus musculus
27	105	2.7	901	5	Q24573	Q24573 drosophila
28	105	2.7	1545	5	Q98H77	Q98H77 leishmania
29	105	2.7	1571	11	Q54978	Q54978 mus musculus
30	105	2.7	2031	5	Q9W918	Q9W918 leishmania
31	104.5	2.7	707	4	Q96SK7	Q96SK7 homo sapien
32	104.5	2.7	806	5	Q9VQK5	Q9VQK5 drosophila
33	103.5	2.7	625	10	Q9FMD7	Q9FMD7 arabidopsis
34	103.5	2.7	924	10	Q9ZVD5	Q9ZVD5 arabidopsis
35	103.5	2.7	1289	11	Q9WTR2	Q9WTR2 mus musculus
36	103.5	2.7	1306	2	Q9L821	Q9L821 enterococcu
37	103	2.7	549	5	Q19655	Q19655 caenorhabdi
38	103	2.7	1156	5	Q967X9	Q967X9 tribolium c
39	103	2.7	1428	5	Q9VU03	Q9VU03 drosophila
40	102	2.7	1448	16	Q8TWJ8	Q8TWJ8 anabaena sp
41	102	2.7	1654	5	Q9VC36	Q9VC36 drosophila
42	102	2.7	4169	4	Q8TCU4	Q8TCU4 homo sapien
43	101.5	2.7	341	6	Q9N0B3	Q9N0B3 macaca fasc
44	101.5	2.7	1639	3	Q9P7Q7	Q9P7Q7 schizosacch
45	101	2.6	539	5	Q9V490	Q9V490 drosophila

#### ALIGNMENTS

#### RESULT 1

Q9UFA0 PRELIMINARY; PRT; 564 AA.  
AC Q9UFA0;  
DT 01-MAY-2000 (TRMBLrel. 13, Created)  
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)  
DE 01-MAY-2000 (TRMBLrel. 13, Last annotation update)  
DE Hypothetical 63.1 kDa protein (Fragment).  
GN DKZP434N1928  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS;  
RA Bloembergen H., Boecher M., Brandt P., Hewes H.W., Gassenhuber J.,  
RA Wiemann S.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; ALI33097; CAB61408.1;  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E88C CRC64;

Query Match 78.5%; Score 3005; DB 4; Length 564;  
Best Local Similarity 99.8%; Pred. No. 5e-268;  
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	155	HPFFFRACDILQPDNLACKPFWKPNLNISQGSQMSQVSPDHPHNGFRFFLYHK	214
Db	1	HPFFFRACDILQPDNLACKPFWKPNLNISQGSQMSQVSPDHPHNGFRFFLYHK	60
QY	215	LKHGSPFRKTCQEQTTTSCLLQVSPGDYIELVDYDNTTKYMYTALAPVSPWA	274
Db	61	LKHGSPFRKTCQEQTTTSCLLQVSPGDYIELVDYDNTTKYMYTALAPVSPWA	120
QY	275	GPRAVAVPLVVISAFATFTVCKKQKQNTSHLDESSSTTTAALPRELRAPR	334
Db	121	GPRAVAVPLVVISAFATFTVCKKQKQNTSHLDESSSTTTAALPRELRAPR	180

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QY 335 PKVFLCYSSGSDONHNNVOCFAIFLQDFCCCEVALDWFDSLCRSGOREMWTOKIHES 394
DB 181 PKVFLCYSSGSDONHNNVOCFAIFLQDFCCCEVALDWFDSLCRSGOREMWTOKIHES 240
QY 395 OFIIVVCSGKMYFVKKNTKHKGGGSGGKGLFVLVAVSAIAELKRAKQSSAALSRF 454
DB 241 OFIIVVCSGKMYFVKKNTKHKGGGSGGKGLFVLVAVSAIAELKRAKQSSAALSRF 300
QY 455 IAYFDYSCGDFVCGIILDLSTKRYLMDNLPLQCLSHLSRDHGLQDFGORTGSGRRNYFR 514
DB 301 IAYFDYSCGDFVCGIILDLSTKRYLMDNLPLQCLSHLSRDHGLQDFGORTGSGRRNYFR 360
QY 515 SKSGSLYVAICNMHQITDEPDMFEKQFVFPHPPLRYREPVLKFDGSLVLDVNCMP 574
DB 361 SKSGSLYVAICNMHQITDEPDMFEKQFVFPHPPLRYREPVLKFDGSLVLDVNCMP 420
QY 575 GPESDFCLAVEAVLGATGADSDHESQGGGLQDGEARPDGDSNAALQPLLETVKAGSP 634
DB 421 GPESDFCLAVEAVLGATGADSDHESQGGGLQDGEARPDGDSNAALQPLLETVKAGSP 480
QY 635 SDMPDSGIYDSSVPSSELSLPLMGLSTDTOTETSSLTSSVSSSGIGGEEPPALPSKILL 694
DB 481 SDMPDSGIYDSSVPSSELSLPLMGLSTDTOTETSSLTSSVSSSGIGGEEPPALPSKILL 540
QY 695 SSGSKADIGCRSTYDELHVAAPL 718
DB 541 SSGSKADIGCRSTYDELHVAAPL 564

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RESULT 2
Q8R5J8 PRELIMINARY; PRT: 582 AA.
AC Q8R5J8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Similar expression to FGF protein (Fragment).
GN SEF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21824237; PubMed-11802165;
RA Furthauer M., Lin W., Ang S.L., Thiasse B., Thiasse C.;
RT "Seif is a feedback-induced antagonist of Ras/MAPK-mediated FGF
signalling."
RL Nat. Cell Biol. 4:170-174(2002).
DR EMBL; AF424604; AAL79530.1;
FT NON_TER
SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

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Query Match 68.3%; Score 2616.5; DB 11; Length 582;
Best Local Similarity 84.6%; Pred. No. 3.5e-232;
Matches 49%; Conservative 34; Mismatches 49; Indels 7; Gaps 4;
QY 136 TDYFVKVFPFPIKSNESYHFFTRACDCLLPDLNACKPFWKPRNLNISQSGSDMV 195
DB 1 TDYFVKVFPFPIKSNESYHFFTRACDCLLPDLNACKPFWKPRNLNISQSGSDMV 60
QY 196 SFDBAPNFGFFVLYHKLKHEGPKRKTCKQETTTSCLLQVSPGDIYIELVDY 255
DB 61 SFDBAPNFGFFVLYHKLKHEGPKRKTCKQETTTSCLLQVSPGDIYIELVDY 120
QY 256 NTRKYVHYALKPVSHPAGPIRAVAITVPLVLSAFATLFTVNCRKQENIYSHLDE 315
DB 121 NTRKYVHYALKPVSHPAGPIRAVAITVPLVLSAFATLFTVNCRKQENIYSHLDE 180
QY 316 SSSSTYALPRELRPRRPFVLCYSSKQGNHNNVQCFATFLQDFGCEVALDWM 375
DB 181 SSSSTYALPRELRPRRPFVLCYSSKQGNHNNVQCFATFLQDFGCEVALDWM 240

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QY 376 PSICREGOREMWTOKIHESOFIIVVCSGKMYFVKKNTKHKGGGSGKGLFVLVAVSA 435
DB 241 PSICREGOREMWTOKIHESOFIIVVCSGKMYFVKKNTKHKGGGSGKGLFVLVAVSA 300
QY 436 IAEKRAKQSSAALSRFIAVFDYSCGDFVCGIILDLSTKRYLMDNLPLQCLSHLSRDH 495
DB 301 IAEKRAKQSSAALSRFIAVFDYSCGDFVCGIILDLSTKRYLMDNLPLQCLSHLSRDH 357
QY 496 GLQDFGORTGSGRRNYFRSKSGSLYVAICNMHQITDEPDMFEKQFVFPHPPLRYFR 554
DB 358 GLQDFGORTGSGRRNYFRSKSGSLYVAICNMHQITDEPDMFEKQFVFPHPPLRYFR 417
QY 555 EPLVLEKFDGSLVLDVNCMPGSPESDFCLAVEAVLGATGADSDHESQGGGLQDGEAR 612
DB 418 EPLVLEKFDGSLVLDVNCMPGSPESDFCLAVEAVLGATGADSDHESQGGGLQDGEAR 477
QY 613 RPAIDGSAALQPLLETVKAGSPDSDHESQGGGLQDGEARPDGDSNAALQPLLETVKAGSP 672
DB 478 RPAIDGSAALQPLLETVKAGSPDSDHESQGGGLQDGEARPDGDSNAALQPLLETVKAGSP 537
QY 673 EYVSSSGIGGEEPPALPSKILLSSGSKADIGCRSTYDELHVAAPL 718
DB 538 EYVSSSGIGGEEPPALPSKILLSSGSKADIGCRSTYDELHVAAPL 582

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RESULT 3
Q8QJ9 PRELIMINARY; PRT: 745 AA.
AC Q8QJ9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE SEF.
GN SEF.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21824236; PubMed-11802164;
RA Tsang M., Friesel R., Kudo T., David I.;
RT "Identification of Seif, a novel modulator of FGF signalling."
RL Nat. Cell Biol. 4:165-169(2002).
DR EMBL; AF364103; AAL76112.1;
FT NON_TER
SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D9DB4 CRC64;

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Query Match 50.9%; Score 1950.5; DB 13; Length 745;
Best Local Similarity 54.1%; Pred. No. 1.3e-170;
Matches 383; Conservative 106; Mismatches 184; Indels 35; Gaps 8;
QY 17 CVANSGVPSRNSGL--YNIYFKDNTTYLFPVGVKRVIAQAQNIITISQYACDQAVT 74
DB 35 CSTKQGTQTSNDGAGKLVGIVFDVDCSVNNPGLKHAHEVNNITFSLSCDSQAAV 94
QY 75 IWSFGALGIEFLKGFVLELSEKSGCQOOLKDKPKOLNSFKRTGMEQFPLNMEF 134
DB 95 VHWASPLGIEHVGAVFVLEKDPNPERKCOHLTKDPRQLNFYKTRKSSQFSSLA 154
QY 135 ETDYFVKVFPFPIKSNESYHFFTRACDCLLPDLNACKPFWKPRNLNISQSGSDMV 194
DB 155 ETDYFVKVFPFPIKSNESYHFFTRACDCLLPDLNACKPFWKPRNLNISQSGSDMV 214
QY 195 VSDHAPNFGFFVLYHKLKHEGPKRKTCKQETTTSCLLQVSPGDIYIELVDY 254
DB 215 VSDHAPNFGFFVLYHKLKHEGPKRKTCKQETTTSCLLQVSPGDIYIELVDY 274
QY 255 TNRKYVHYALKPVSHPAGPIRAVAITVPLVLSAFATLFTVNCRKQENIYSHLDE 314
DB 275 TNRKYVHYALKPVSHPAGPIRAVAITVPLVLSAFATLFTVNCRKQENIYSHLDE 334

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QY 315 ESSESSTYTAALPRELRLPRKPVLCYSKQGNMNVQCFAYFLQDFCCCEVALDLME 374  
 DB 335 ESSESSTYTAALPRELRLPRKPVLCYSKQGNMNVQCFAYFLQDFCCCEVALDLME 394  
 QY 375 DFSICRGQREWIYQIHESOFIIVVCSKGMFYVDKKNYKHGGGR-----GS 423  
 DB 395 HLEICKEGOMSLSRIDEAHEFIITVCSKGLHFVKEHRKKGATSKENREPSADSS 454  
 QY 424 GKGELELVAVSAIAELKROAKQSSAALSKFYAVFYDSCGVDVPGILDLSKYRLMDNL 483  
 DB 455 SSRLDLIVASAIISKEKVEHQSS-DLSRFMSVYFDYSHETDPTSLAPKFKMDQL 513  
 QY 484 POLCSHLHSDRGLOEQHTRGSRNFRSKSGSLYVAICNMHOFIDEPDWEKOF 543  
 DB 514 POLFAELHBRQLSLDREPPQPNVSKRNTFCSGSLYVAIYNMHQVTOEPDWEKEL 573  
 QY 597 SOHESQBGGLDQGEARPALDGSAALOPLHVTAGSPDMRDSGIDSSVSPSELSLP 656  
 DB 630 SREDLGSGSSQD-----AGSCRPLVLTGDSAGSPDMRDSGIDSSVSPSELSIP 680  
 QY 657 LMEGLSTDTOTETSSITSSVSSSGLGCEPPALPSKILLSGS-CKADL 703  
 DB 681 LMDGLSPDHADNSLADSVSSSGLGDEPPAVVSLHCTANTICKADL 728

## RESULT 4

ID Q8QJ16 PRELIMINARY; PRT; 745 AA.  
 AC Q8QJ16;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE FGF signaling antagonist Sef.  
 GN SEF.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21824237; PubMed-11802165;  
 RA Fuerthauer M., Lin W., Siew-Lau A., Thisse B., Thisse C.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF401232; AAF78817.1;  
 SQ SEQUENCE 745 AA; 83437 MW; 75BB9DCC08A4652 CRC64;

Query Match 50.7%; Score 1941.5; DB 13; Length 745;  
 Best Local Similarity 53.8%; Pred. No. 8.7e-170;  
 Matches 381; Conservative 108; Mismatches 184; Indels 35; Gaps 8;

QY 17 CVANEGVGPASRNSGL--YNTFFKDYNTYLPVKGKVIADAQNTISQYACHQVAVT 74  
 DB 35 CSTYGGTQTSMDDEGARKLVGTFRIDNCVNNVSPGLKRAIHEVNNISFSLSCDSQAVV 94  
 QY 75 IAWSPGALGIEFLKGRFVILEELKSEGRQCOQLIKADPKQLNSSFRTGHSQPLANKF 134  
 DB 95 VHNMAASPLIGIEHVKGRFVYLEDKPNRKOCHILKADPKQLNSSFRTGHSQPLANKF 154  
 QY 135 ETDYFVKVPPSPKSNHYPFFRTRACDILQADPNLCKPFWKPRNLTISQHSQDQ 194  
 DB 155 ETDYFVKVPPSPKSNHYPFFRTRACDILQADPNLCKPFWKPRNLTISQHSQDQ 214

QY 195 VSDHAPHNCFPRFYLKLEKGGPFKFKCKOBOTETTCTTCLHQNVPDGIYIELVDD 254  
 DB 215 VYDHPSTFGESYIYIKLRGEGFRLKCKEPONGPTTCVLDQVTPGTALIELRDD 274  
 QY 255 TWTRKVMETALKPVHSPAGPIRAVATVPLVVISAFATLFTVWCRKQENIISHLE 314  
 DB 275 SNTRRQTOHYVSQVHSPAGPIRAMATVPLVVISAFATLFTVWCRKQENIISHLE 334  
 QY 315 ESSESSTYTAALPRELRLPRKPVLCYSKQGNMNVQCFAYFLQDFCCCEVALDLME 374  
 DB 335 ESSESSTYTAALPRELRLPRKPVLCYSKQGNMNVQCFAYFLQDFCCCEVALDLME 394  
 QY 375 DFSICRGQREWIYQIHESOFIIVVCSKGMFYVDKKNYKHGGGR-----GS 423  
 DB 395 HLEICKEGOMSLSRIDEAHEFIITVCSKGLHFVKEHRKKGATSKENREPSADSS 454  
 QY 424 GKGELELVAVSAIAELKROAKQSSAALSKFYAVFYDSCGVDVPGILDLSKYRLMDNL 483  
 DB 455 SSRLDLIVASAIISKEKVEHQSS-DLSRFMSVYFDYSHETDPTSLAPKFKMDQL 513  
 QY 484 POLCSHLHSDRGLOEQHTRGSRNFRSKSGSLYVAICNMHOFIDEPDWEKOF 543  
 DB 514 POLFAELHBRQLSLDREPPQPNVSKRNTFCSGSLYVAIYNMHQVTOEPDWEKEL 573  
 QY 544 VPFPPLPRYREPLYLEKEDSGVLNDVCKPGPSDFCLKVEAVL-----GATPAD 596  
 DB 574 M---PPPLPKETIPEKYVDVSGVLNVEKLGEGSE-CPPVRSNVLLIPOTPVGVVSL 639  
 QY 597 SOHESQBGGLDQGEARPALDGSAALOPLHVTAGSPDMRDSGIDSSVSPSELSLP 656  
 DB 630 SREDLGSGSSQD-----AGSCRPLVLTGDSAGSPDMRDSGIDSSVSPSELSIP 680  
 QY 657 LMEGLSTDTOTETSSITSSVSSSGLGCEPPALPSKILLSGS-CKADL 703  
 DB 681 LMDGLSPDHADNSLADSVSSSGLGDEPPAVVSLHCTANTICKADL 728

## RESULT 5

Q9NA64 PRELIMINARY; PRT; 846 AA.  
 ID Q9NA64;  
 AC Q9NA64;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Y64G10A.6 protein.  
 GN Y64G10A.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ainscough R.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99069613; PubMed-9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology".  
 RL Science 282:2012-2018(1998).  
 DR EMBL; AL110498; CAB54470.1;  
 SQ SEQUENCE 846 AA; 94852 MW; 613AEF5EBB89EA4 CRC64;

Query Match 4.5%; Score 170.5; DB 5; Length:846;

Best Local Similarity 21.4%; Pred. No. 2e-06; Indels 211; Gaps 37;  
Matches 141; Conservative 82; Mismatches 225;

QY 64 QYACHQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLIKADPKQLNSSFRTG 123  
 DB 294 QY-CFEYEVRLDGS---GIVMLQSAITIKDELATE-----IINGRPVQGEF----- 338  
 QY 124 MESQPLMKKEFTDYVAVVVPFSPKSNHYPFFRTRACDILQADPNLCKPFWKPR 182



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DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD_1.
DR Pfam: PF00271; Helicase_C_1.
DR SMART: SM00490; HELICC; 1.
KW ATP-binding; Helicase.
FT NOTED
SQ SEQUENCE 757 AA; 84382 MW; 1AE1EA14435382A7 CRC64;

Query Match 3.18; Score 117; DB 3; Length 757;
Best Local Similarity 20.48; Pred. No. 0.15;
Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;

QY 233 ETTSCLQNSPGDYIIIEVDLNTTRKVMYALKPVHSPWAGPIRAV-----ATTVPL-- 286
DB 77 ETTLILPTVALRANMLAKLDVNN-----IRYHVQP-GSGAAPIVLVSTAAITLAPKE 131
QY 287 -----VVISAFATLFTVMCKKQENIYSHLDEESSESTYTAALP----- 327
DB 132 YANRLOQQLRQRIYDCHTLTARSYRSNQLANHYDVDTQTWTLTLPPEZDA 191
QY 328 -----RERLRPRKVF-----LCYSKQGNENNVVQCF-AYFLDFGCEVALDWEDF 376
DB 192 FISHNKLTPILIVRESTNRSNLCISVTAETHRMGMTCYDAVRVD---ECRAETDIW--- 246
QY 377 SLREGQRENVIOKTHESQFIIVVCSKGMKYEVDK-----KNYKHGGGRGS----- 423
DB 247 -----NGQD-----RIIVYCTSS--KELVARIAELMGLCAAISSESGEADKAAIIQ 290
QY 424 ---GKGLFLVAVSAIAELKRAOKOSSAALSKEFIATYFDYSCGDVPGIL--DLSTKY 477
DB 291 DWICGKSPVIVATSA-----LVGFDYFHVRFVILLGLPDLTDF 331
QY 478 -----RLMDNLPOLCSHLHSHDGLQEPQHQRRSRRNFRS 515
DB 332 SQESGRAGRGHPAESILLAGPQLDRAP-ASGRASSAERKGVAPG--ADKEMAQIYRS 397
QY 516 KSGSLTVACNMHOFIDEEPWFQKQFVFPHPPPLRYREPLEKEDSLVINDVCKPG 575
DB 388 RK-----YCLRGVLSQLQDRSDW-----RWCHGEGQLCSVC 419
QY 576 PESDFCLKVAZAVLGATGPADSOH---ESQHGGLDQCEGARPALDGSAAALPILHTYKAG 632
DB 420 PGHFF-----QARGPGQGFHTAPAQAGDPSTQGRHPSMHGSS--HPSNH----- 463
QY 633 SPSPMDRSDGIYDSSVPSSE--LSLPLMEGLSTDQETSSLTSESVSSS---SGLGREPPA 688
DB 464 -----GSSHPSSGSSHPSTHGSSHPSTHGSS--RPSIHGSGQHGQRRKQDPD 510
QY 689 LPSK 692.
DB 511 PPSE 514

RESULT 8
Q9KE04 PRELIMINARY; PRT; 901 AA.
ID AC Q9KE04
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transposase (08)/ABC transporter (ATP-binding protein).
GN BH1054
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;

RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
RL halodurans and genomic sequence comparison with Bacillus subtilis.*;
RE Nucleic Acids Res 28:4317-4331(2000)
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC -2- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
DR EMBL: AF001510; BAB04773.1;
DR InterPro: IPR003593; AAA_Atpase...
DR InterPro: IPR003439; ABC_transporter...
DR Pfam: PF002559; Transposase_11.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF01609; Transposase_11; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 901 AA; 104585 MW; E519406E50B2CBB CRC64;

Query Match 3.08; Score 116.5; DB 16; Length 901;
Best Local Similarity 19.68; Pred. No. 0.21;
Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY 26 ASRNSGLNITFKYDNCITLYNPVGHVIAQAQNTISQY-ACHDQAVATILMSPGALGI 84
DB 333 ALKESGL-----PLPKTLADAGTGSNTYVAMADELFTLIPS----- 371
QY 85 EFLKGRFVILELSEGR-----QQOQL--ILKDPKQLANSFKRTGMSQPLNMF 134
DB 372 ---HTFR--QEQKSPAKRFPYINWRCDDTDVTCNPQRKVSFKRTKTDY--GY 423
QY 135 ETDYFV-----KVVP-PSI-----KNESNTHPEFFTRACDILLQDNLCKPMPKR 182
DB 424 ARDFVTECECECPKFPCTKAGNRQVHNPV-----EELKAKOHOKLK 471
QY 183 NLNISQHG-----SDMQVSDHAPHFQFRFPYLHKLKHGEPFRKTKAQETTER 234
DB 472 ---SEEGTLYQKRTDVSFVGHVKONLGRFLHLGR----- 507
QY 235 TSCLLQNVSPGDIYIELVDNTTRKVMYALKPVHSPWAGPIRAVATVPLVVIS-AFA 293
DB 508 -----ESVHIELGLVALHNLR 524
QY 294 TLFVTKRCKQENIYSHLDEESSESTYTAALPRELRPRKRVFLCYSSKDGQGNMNV 353
DB 525 KRATVDRRSEKPTNQHKNR-----RIKRF-----SREYVL 558
QY 354 QCF---AYFLADFQCGEVALDWEDFSICRSGQREWY---LOKHESQFIIVVCSKGMK 406
DB 559 RCWDSPPFIKSDGQVAFALFD--KLREGEENMIEVIDLSKTYRNQVY---KGIN 612
QY 407 YFDKNTKHKGGGSGKGELELVASAI-----AKLQAKQSSSAALS 453
DB 613 MFERGENVGLLGPNGAKSTTISMISSLIQPTSGDVILKGGSIHQSKALRSILGVVPQ 672
QY 454 FIATYFDYSC-----GDVPGILDSTKYLMDNLPCZLSHLSHSDGLQEPQHQRRQ 507
DB 673 EIAVTDLTARENLAFFKTYGLKGLAKHR-NESTLIQV-----GLEE-----RON 718
QY 508 SRENYRSKSGSLYVAICNNHQ---FIDEPE 536
DB 719 DRVTFSGGMRRLNIAVALLHEPELIIMDEP 750

RESULT 9
Q99754 PRELIMINARY; PRT; 549 AA.
ID AC Q99754
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC
DE 2.7.1.68).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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QY 617 DGSAAQLPHTVVKAGSDMPDROGLYSSVP---SSELSPLMAGLSTDTQTSRLTE 673  
 DB 266 PAAA-----GGGAGSPRTSRVSG--HTKIPDESEVTSASKEJGR-OPGRPHRE 317  
 QY 674 SVSSSSGLG-KEEPPALPSKLLSGSCKA 701  
 DB 318 AAQDPGSGSEOPSAAPSLRAAPSCSS 346

RESULT 12  
 Q9NTU6 PRELIMINARY; PRT; 428 AA;  
 AC Q9NTU6  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 15, Last annotation update)  
 DE Hypothetical 45.4 kDa protein.  
 GN DXPFX347211.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RX MEDLINE=11154917; PubMed=11230166;  
 RA Wiseman S., Weill B., Wellenreuther R., Gassenhuber J., Glassl S.,  
 RA Ansgore W., Boecker H., Bloeker H., Bauersachs S., Blum H.,  
 RA Lauber J., Oesterwehlt A., Beyer A., Koehler K., Strack N.,  
 RA Meves H.W., Oesterwehlt B., Obermaier B., Tampe J., Heubner D.,  
 RA Wambutt R., Korn B., Klein M., Poustka A.,  
 RT Towards a catalog of Human genes and Proteins: Sequencing and  
 RT Analysis of 500 Novel Complete Protein Coding Human cDNAs.  
 RL Genome Res. 11:422-435(2001).  
 DR EMBL; AL117401; CAB5902.2;  
 KW Hypothetical protein.  
 SQ SEQUENCE 428 AA; 45443 MW; FA75BAC1A3FDB3EE CRC64;

Query Match 2.9%; Score 110; DB 4; Length 428;  
 Best Local Similarity 23.5%; Pred. No. 0.27;  
 Matches: 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 439 KLRQAKSS-SAALSKEFIAVDFSCGDPVGI-----LQSTKRLMDNLPQ 485  
 DB 103 RYNTQTSQTSCTNRNAISSVSTGGPLGLRRGPPASSHCQLTLSSKTSVEDRPQ 162  
 QY 486 LCSHLERSDGLQE--PGQHTQSGRENTFRSGSLYVAICNMQPIDEQPKWFKQF 543  
 DB 163 AVSSCHTQCEKADIAQGLT--LRNDSSTSEASP-----STHF-----PLIPRRG 210  
 QY 544 VPFH-PPPL-----RYREPVLEKFGSLVLDVM---CKPGSPDFCLKVEAA 587  
 DB 211 EPLMLPPELGRVTVVDREKAAAFQINSALQVEDKAIQDPRSPSH---TLSSL 267  
 QY 588 VIGATG-PADSQHESQHGGLQDGEARPDALDQSAALQPLHTVKAQSPDMP-----RD 640  
 DB 268 ATGASGLPAVSKAPS-----MQAQETKSDCIGLGLDPLASA--AGVPSTAPMSCKERP 321  
 QY 641 SG-ITDVSVPSSSELSPLMAGLSTDTQTSRLTESVSSSGSLGEEPPALPSKLLSGG 697  
 DB 322 PGLPSSSDP-----LPATSSDSQDSQAQVTSLI-----PAPPAASHDAG 361

RESULT 13  
 Q81789 PRELIMINARY; PRT; 917 AA.  
 AC Q81789  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 101.6 kDa protein.  
 GN F8D20.70 OR AT4G35560.

OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosid1; Brassicales; Brassicaceae; Arabidopsi  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Koettler P., Hempel S., Entian K.-D., Hohelsel J., Jesse T.,  
 RA Heljehn L., Vos P., Meves H.W., Mayer K.F.X., Schueller C., Bevan M.,  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rose M., Hempel S., Entian K.-D., Meves H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL; AL031135; CAA20026.1;  
 DR EMBL; AL161587; CAB80272.1;  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00400; WD40; 2.  
 KW Hypothetical protein; Repeat; WD repeat.  
 SQ SEQUENCE 917 AA; 101552 MW; 1809BDC42302C820 CRC64;

Query Match 2.9%; Score 110; DB 10; Length 917;  
 Best Local Similarity 18.1%; Pred. No. 0.87;  
 Matches: 154; Conservative 124; Mismatches 281; Indels 292; Gaps 37;

QY 24 GPASR-----NSGLNITFKYDNCVTILNPVGHV---TADAQNT--TISQACHDOVA 72  
 DB 148 GKASRVTVGSSNSLSQVLLNQETETRAKILGLVSEPCADMEILADVNESKHQDF 207  
 QY 73 VTILNPGALGT--EFLAGFRVILELASQEQOQILIDPKQLNSFKRTGHSOP-- 128  
 DB 208 LFLVIGSGRYAIDDIEMIEKLIQSQSSPSLPRTVVKLPFSQSSITVGFELRPSPH 267  
 QY 129 FLAKKFTDY-----FKVVPFPPSIKNESN---YHPFF-----FRACDQLLQDNL 173  
 DB 268 LLNLSDSE-DYALAKADAVPFLPFTPTPKSSSAHFPGFTKVNVTITGHCDGISWDM 326  
 QY 174 ACK-----PFMKPR-NLMSIQG-----SDMQVSDFAHPHGFGRFFLYLKL 215  
 DB 327 TCSFPLVLFLKEQIDQDVSRGNMAALTALHYDSNRLVSGDHNGKRLYRFPKPEYLT 386  
 QY 216 KH-----EGPFR-----KCKQEQTTTTCILQWSP-----QDYIELVDD 254  
 DB 387 ENSFIPQSLAKGNHIVQSVYIKLTGSIICQKSONSKHLAIGSDQGHDSLVEID- 445  
 QY 255 TMTTRVMYALKPVHSWACQTRAVATVPLVTSAPALFT----- 297  
 DB 446 -----ALTPY-----LQVSLVDEANVLTITKHASIDICPGIISQFE 484  
 QY 298 -----VNCRKQOENIYSHLDEESSESTYTAALPRELRPRKPVLCYSSKQDG 347  
 DB 485 SCIVQGFENLVAVARRDSVFA-LQSDTGNMIGTNMKPK-----KPKVLYHQILLDGK 538  
 QY 348 NNNNVQCFAYFLQDFCCCEVALDLNDFELSCREQREWIKIHESQFIIVGCS----- 402  
 DB 539 -----QDTSG-----NGDTSRES-----TVEISITRQPSVLVCSKAIY 573  
 QY 403 -----KGMKVFYDKNKYKHKG-----GGGSGKGLFLVAVSAIAE-----KLR 441  
 DB 574 IYSLARVQGVTKVLEKAKFSPPICSASTFTGSGVG---LTLVDTCTVEISLPELS 630  
 QY 442 QAKOS-----SSAALSKEFIAVDFSCGDPVGI-----LQSTKRLMDNLPQ 483  
 DB 631 QLKQTSIRGFTYSSPKPSLPEITISASWDGDLVNVNGDDELIVSVLPQKTRFLVESH 690  
 QY 484 POLCSHLERSDGLQEAPQHTQSGRR-----NYFRSKSGSLYVAICNMQPIDEQPD 537  
 DB 691 -----NRVIKIDNSVCHGIIITSSPREKKSMPGSKVTKSKRTDTPEPSSKTEIELSK 746

QY 538 WPKQFVP-----HPPPLRVPPVLEKFDGSL 565  
 DB 747 IFSTANFNANNVENSEINTVRYVEDEELDIDDHPNQQOQKPEKQGISL 806  
 QY 566 -----VLNDVCKKPPSPDCLKVAEVLGAGPADSCHESQGGI-----DQ 608  
 DB 807 SKOKANRPNFKKQKMAKNEKSV-----TNDEKHEKNGAVDQIKKKYGFSSDE 862  
 QY 609 DGEARPDGSAALQPLLLHTRVAGSPDPRSGIYDSSVPSSELSPLMEGLSTQDT 668  
 DB 863 MGAARMA-----QSKLOD-----NLKQIGISLATTEM 890  
 QY 669 SSLTESVSSSS 679  
 DB 891 EDFAKSFSTA 901

## RESULT 14

Q95WA7 PRELIMINARY; PRT; 903 AA.  
 AC Q95WA7;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Putative clock protein period.  
 GN PER.  
 OS Bulla gouldiana (California bubble).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia;  
 OC Cephalaspidea; Bullidae; Bulla.  
 OX NCBI\_TaxID=114738;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Constance C.W.  
 RT "Cloning and analysis of clock genes in the marine mollusc, Bulla gouldiana."  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF353619; AK97374.1;  
 DR InterPro; IPR001610; PAC.  
 DR Pfam; PF00989; PAS; 2.  
 DR SMART; SM00086; PAC; 1.  
 SQ SEQUENCE 903 AA; 101146 MW; 22BD87376BC5324A CRC64;

Query Match 2.8%; Score 108; DB 5; Length 903;  
 Best Local Similarity 19.9%; Pred. No. 1.3;  
 Matches 115; Conservative 62; Mismatches 223; Indels 178; Gaps 27;

QY 214 KLAHEGPKKTKCKOQTTSTCLQNVSPGDYILLYDVTNTRKYNH-YALKPVHSP 272  
 DB 83 KLASVLPKERTGN-----DTLSLEQ-----LYNSKQINBEKRYEHEFTPPHS- 130  
 QY 273 WAGPIRAVAVPLVLSAFATLFTVCKKQENYTHLDESSSTYTAALPRERLR 332  
 DB 131 -----GSPHSDGKELSQSEMITYMTLKNVVGUTASPPPLHGLY 170  
 QY 333 P-----RPKVFICYSKDQHNHNVQCFAYLQPCGCEVALDWFSLCRBQREWI 388  
 DB 171 PVDWNRGLLDKFNKKDMNTLN--SCIARYSTD-----EAADNFES-----SNCTR----- 215  
 QY 389 QKHESQFTIVVCKGKMYVDK-KNYKHGGGKSGCKGLFLVAVSAIAKLRQAKS- 446  
 DB 216 -----VTEGSKYFTARRIRREKLGSGFSLQNVSCFPMMSKTVLSELS 264  
 QY 447 -SSAALSKEFIAYFD-----YCEGDPVCLDLSTKY-----RLMDNLRL 486  
 DB 265 EDGVRVRESLVLCNPKNSAINGGLDKNFSLRHSFCNTYTAHNAVLLGLPLD 324  
 QY 487 CSHLSRDRGLQEP-----GHTROGSRNFRFSKGRSLYA----- 524  
 DB 325 FSGMSTFD-LYHPDDFQQLDTHIRIMLSMGOPFKSGS-----ILKTRNGCYVEVTEM 378  
 QY 525 -----ICNMHQFI--DEEPDWFKEQVFPFPPPLNYREPVLKFDGSLV--- 566

DB 379 SSENPNKSELEFLIGHTVILKGTNFEDFED-LPSRDEKFEF-SPELKIOEKIVEL 435  
 QY 567 ---LNDVCKKPPSPDCLKVAEVLGAGPADSCHESQGGI-----DQ 608  
 DB 436 KPIQSTVFAEP-----PYAAQTQVPPQQAQIVTQ-----TAPVQSPAARE 480  
 QY 624 PLLHTRVAGSPDPR-----DSGI-----YDSSVPSSELSPLMEGL 661  
 DB 481 PAEPAPK--PPSEKSKVATTEKGSVIDDKGSIYINOLNYSHNKIRFLNSHP--KSF 536  
 QY 662 STDOTETSSITSSVSSSGAGREPPALPSKILSSGSC 699  
 DB 537 SNVSDSVVTRDSEDAINDEEMPLEIPVVKPPSC 574

## RESULT 15

Q9AY10 PRELIMINARY; PRT; 1058 AA.  
 AC Q9AY10;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Putative gag-pol. polyprotein.  
 GN OSJNHA0087H07.4.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,  
 Kim H.-R., Rambo T., Henry D., Simmons J.,  
 \*Rice Genomic Sequence.\*  
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AC074283; AAK02020.2;  
 DR Polyprotein.  
 SQ SEQUENCE 1058 AA; 115228 MW; 9E39B2C56AFC6CE7 CRC64;

Query Match 2.8%; Score 108; DB 10; Length 1058;  
 Best Local Similarity 22.1%; Pred. No. 1.7;  
 Matches 85; Conservative 52; Mismatches 131; Indels 116; Gaps 21;

QY 416 HGGGGRSGKGLFLVAVSAIAEKL-----ROAKSSSALSKEFLAV-- 457  
 DB 204 NRGSGGRGKDGKPKPTCQCGKVGHTVAKWKFRDPSPFTREKSKRTAATSSSYGIDT 263  
 QY 458 --YDYSCGDPVCLD-LSTKYRLMDNLQCLCSHLSRDEGLQPCGHTROGSRNRY-- 512  
 DB 264 WYVDSNATDHIIGEMKLSVKDYKGS-----EYVHAGCTGHEDANPAROPNLRYNH 318  
 QY 513 -----PRSKSGSLVIAICMHQ-----FIDEPPWFKEQVFP--HP-PPLR 552  
 DB 319 RKLFRSK--QCAPLGYSTLHGFKCLDSTGRVYISRDV-VFDEQIYFANLHPNAGAR 375  
 QY 553 YREPYL-----EKFD-SGLVNDVCKKPP-----ESDFCLKYE 585  
 DB 376 LRSYLVLPDLLPPTQFGGAIYNDOPMIDDPNHTNOTAETDADRGAQVNSEPTGENN 435  
 QY 586 AVALGATGP-----ADQSCHESQGGIADGEARPDGSAALQPLLATVAG----- 632  
 DB 436 ASNGGTEPKGHDPMHGTSSGSGGQHTGSHPEDDAAASVASA-----ESGNDTGT 487  
 QY 633 SPSPDPRSG-IYDSSVPSSELSPLMEGLSTQDTETSSITSSVSSSGSL-----GREEP 687  
 DB 488 SPACGTGANGHESQGESSTISAP-----HDSFSASTPGSDASDGVESGGQQOP 540  
 QY 688 AL-PSKILSSGSCADLGCRTYTD 710  
 DB 541 MLGPATRSRHGHGHP-----KRYTD 560

Mon May 19 09:52:44 2003

us-09-912-157-2\_copy\_36\_753.rspt

Page 9

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Job time : 63.3267 secs



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 09:07:58 : Search time 31.4416 Seconds  
(without alignments)  
1771.498 Million cell updates/sec

Title: us-09-912-157-2\_COPY\_336\_753

Perfect score: 2210

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Scoring table: BLOSUM62 Gap 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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8:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1987.DAT.1	2210	Human Interleukin
9:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1988.DAT.1	2210	Human Interleukin
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15:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1994.DAT.1	2210	Human Interleukin
16:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1995.DAT.1	2210	Human Interleukin
17:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1996.DAT.1	2210	Human Interleukin
18:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1997.DAT.1	2210	Human Interleukin
19:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1998.DAT.1	2210	Human Interleukin
20:	/SID22/gcgdata/geneseq/genesecp-emb1/AA1999.DAT.1	2210	Human Interleukin
21:	/SID22/gcgdata/geneseq/genesecp-emb1/AA2000.DAT.1	2210	Human Interleukin
22:	/SID22/gcgdata/geneseq/genesecp-emb1/AA2001.DAT.1	2210	Human Interleukin
23:	/SID22/gcgdata/geneseq/genesecp-emb1/AA2002.DAT.1	2210	Human Interleukin

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2210	100.0	728	AAU04958	Human Interleukin
2	2210	100.0	738	AAU11355	Human DNAX cytokine
3	2210	100.0	739	AAU10602	Human Interleukin
4	2210	100.0	739	ABE07628	Human cytokine rec
5	2210	100.0	733	ABE07626	Human cytokine rec
6	2206	99.8	753	ABE07627	Human cytokine rec
7	2201	99.6	738	AAU09904	Human Interleukin
8	2201	99.6	738	AAU09951	Human Interleukin
9	2201	99.6	738	AAU09952	Human Interleukin
10	2197	99.4	738	AAU09953	Human Interleukin

11	2196	99.4	738	22	AAU09954	Human Interleukin
12	2194	99.3	738	22	AAU09956	Human Interleukin
13	2190	99.1	738	22	AAU09955	Human Interleukin
14	2190	99.1	738	22	AAU09957	Human Interleukin
15	1813.5	82.1	739	23	ABE07630	Murine cytokine re
16	984.5	44.5	554	23	AAU91330	Human novel secret
17	310	14.0	866	17	AAW04185	Human Interleukin
18	310	14.0	866	19	AAW04185	Human Interleukin
19	310	14.0	866	20	AAW92409	Human IL-17R prote
20	310	14.0	866	21	AAW92409	Human IL-17R prote
21	310	14.0	866	21	AAW92409	Human Interleukin
22	310	14.0	866	21	AAW92409	Human Interleukin
23	310	14.0	866	21	AAW92409	Human Interleukin
24	310	14.0	866	21	AAW92409	Human Interleukin
25	310	14.0	866	21	AAW92409	Human Interleukin
26	289.5	13.1	864	17	AAW04184	Human Interleukin
27	289.5	13.1	864	19	AAW04184	Human Interleukin
28	289.5	13.1	864	20	AAW92408	Human Interleukin
29	289.5	13.1	864	21	AAW92408	Human Interleukin
30	289.5	13.1	864	21	AAW92408	Human Interleukin
31	289.5	13.1	864	21	AAW92408	Human Interleukin
32	289.5	13.1	864	21	AAW92408	Human Interleukin
33	289.5	13.1	864	21	AAW92408	Human Interleukin
34	289.5	13.1	864	21	AAW92408	Human Interleukin
35	271.5	12.3	539	23	AAW47457	Human IL-17R recept
36	132.5	6.0	238	20	AAW31624	Human IL-17R recept
37	127.5	5.8	191	21	AAW31624	Human IL-17R recept
38	127.5	5.8	286	23	AAW47457	Human IL-17R recept
39	127.5	5.8	385	21	AAW31624	Human IL-17R recept
40	127.5	5.8	385	22	AAW31624	Human IL-17R recept
41	127.5	5.8	385	23	AAW47457	Human IL-17 recept
42	127.5	5.8	502	22	AAU09953	Human PRO polypept
43	127.5	5.8	502	22	AAU09953	Human EST encoded
44	127.5	5.8	502	22	AAU09953	Human Interleukin
45	127.5	5.8	502	22	AAE06586	Human protein havi

ALIGNMENTS

RESULT 1

ID AAU04958 standard; Protein; 728 AA.

AC AAU04958;

XX (first entry)

DE Human Interleukin 17 receptor, IL-17RH4.

Human Interleukin-17 receptor; IL-17RH4; agonist; antagonist;

PRO20026; DNA 154095-2998; systemic lupus erythematosus;

rheumatoid arthritis; Osteoarthritis; diabetes mellitus;

allergic disease; asthma; demyelinating disease;

degenerative cartilaginous disorder; transplantation associated disease.

OS Homo sapiens.

Key	Region	Location/Qualifiers
FT	Modified-site	19..24 "N-myristoylation site"
FT	Modified-site	31..34 "Asn is N-glycosylated"
FT	Modified-site	38..41 "Asn is N-glycosylated"
FT	Modified-site	56..59 "Asn is N-glycosylated"
FT	Modified-site	113..116 "Asn is N-glycosylated"
FT	Modified-site	147..150 "Asn is N-glycosylated"
FT	Modified-site	182..185 "Asn is N-glycosylated"
FT	Modified-site	182..185 "Asn is N-glycosylated"

Region: 232..235  
 /note- "cAMP/GMP-dependent protein kinase phosphorylation site"  
 Modified-site: 266..269  
 /note- "Asn is N-glycosylated"  
 Domain: 283..307  
 /note- "transmembrane domain"  
 Region: 312..319  
 /note- "Tyrosine kinase phosphorylation site"  
 Region: 375..380  
 /note- "N-myristoylation site"  
 Region: 416..424  
 /note- "Tyrosine kinase phosphorylation site"  
 Region: 428..433  
 /note- "N-myristoylation site"  
 Region: 429..434  
 /note- "N-myristoylation site"  
 Region: 432..437  
 /note- "N-myristoylation site"  
 Region: 433..436  
 /note- "N-myristoylation site"  
 Region: 517..522  
 /note- "glycosaminoglycan attachment site"  
 Region: 574..578  
 /note- "N-myristoylation site"  
 Region: 652..657  
 /note- "N-myristoylation site"  
 Region: 707..712  
 /note- "N-myristoylation site"  
 WO200146420-A2.  
 28-JUN-2001.  
 20-DEC-2000; 2000WO-US34956.  
 23-DEC-1999; 990S-0172096.  
 30-DEC-1999; 990S-US31276.  
 11-JAN-2000; 2000US-0174481.  
 18-FEB-2000; 2000WO-US30434.  
 02-MAR-2000; 2000WO-US03841.  
 21-MAR-2000; 2000US-0191007.  
 21-MAR-2000; 2000WO-US07532.  
 02-JUN-2000; 2000WO-US15264.  
 22-JUN-2000; 2000US-0213087.  
 22-AUG-2000; 2000US-0644848.  
 24-OCT-2000; 2000US-0242837.  
 10-NOV-2000; 2000WO-US30873.  
 28-NOV-2000; 2000US-0253646.  
 01-DEC-2000; 2000WO-US32678.  
 (GENE ) GENENTECH INC.  
 Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Li H, Hillan KJ, Tamas O, Van Lookeren M, Vandlen RL, Watanabe CK, Williams PM, Wood WL, Yansura DG;  
 WPI; 2001-451708/48.  
 N-PSDB; AAS09517.  
 Novel PRO polypeptides homologous to interleukin-17, useful for the diagnosis and treatment of immune related disease e.g. rheumatoid arthritis and diabetes  
 Claim 10; Fig 18; 18pp; English.  
 The sequence is PRO20026 which is the human Interleukin 17 receptor, IL-17RA4, encoded by DNA 134095-2996. A composition containing antiagonists to the PRO polypeptides or individual components are useful for treating a mammal with an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy; Sjogren's syndrome, systemic vasculitis, sarcoidosis; autoimmune hemolytic anaemia, autoimmune thrombocytopenia; thyroiditis, diabetes mellitus, immune-mediated renal disease; a demyelinating disease, an autoimmune or immune-mediated skin disease, contact dermatitis, an allergic disease e.g. food hypersensitivity, asthma, a transplantation associated disease, or a chronic inflammatory demyelinating polyneuropathy. Treating a degenerative cartilaginous disorder comprises administering a PRO1031 or PRO1122 polypeptide-agonist, or antagonist to the mammal. Numerous examples of the diseases and disorders are given in the specification.  
 XX  
 SQ Sequence 728 AA;  
 Query Match 100.0%; Score 2210; DB 22; Length 728;  
 Best Local Similarity 100.0%; Pred.No: 1.7e-210;  
 Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RKQENIYSHLDESSSTVTAALPRRLPRKPVFLCYSSKDGQENHNVVQCFAYFL 60  
 Db 311 RKQENIYSHLDESSSTVTAALPRRLPRKPVFLCYSSKDGQENHNVVQCFAYFL 370  
 QY 61 QDFCGCVALDWEFSLCRQSGREWIQKHESQPIIIVCSKGMKYFDVKNYKHGGG 120  
 Db 371 QDFCGCVALDWEFSLCRQSGREWIQKHESQPIIIVCSKGMKYFDVKNYKHGGG 430  
 QY 121 RSGSGELFLVAVSAIAEKLQAKQSSAALSFAVTFDYSCGDPVGLDLSKYRLM 180  
 Db 431 RSGSGELFLVAVSAIAEKLQAKQSSAALSFAVTFDYSCGDPVGLDLSKYRLM 490  
 QY 181 DNLPLQCSHLSDHGLQPGQHTROGSRNTFRSKGSLTYVAICNHQFIDEEPWF 240  
 Db 491 DNLPLQCSHLSDHGLQPGQHTROGSRNTFRSKGSLTYVAICNHQFIDEEPWF 550  
 QY 241 KQFVPEPPRLYREPVLEKESGLVNDVCKKGPESDCLKYRAVILGATGADSOHE 300  
 Db 551 KQFVPEPPRLYREPVLEKESGLVNDVCKKGPESDCLKYRAVILGATGADSOHE 610  
 QY 301 SOHGLDQDGEARPAIDGSAALQPLLETVRAGSPDMRDSGIYDSSVPSSELSPLMEG 360  
 Db 611 SOHGLDQDGEARPAIDGSAALQPLLETVRAGSPDMRDSGIYDSSVPSSELSPLMEG 670  
 QY 361 LSTDQTETSLTESVSSSGSGEGEPPALPESKLLSSGSKADLCRSYITDELHVA 418  
 Db 671 LSTDQTETSLTESVSSSGSGEGEPPALPESKLLSSGSKADLCRSYITDELHVA 728  
 RESULT 2  
 AA011355  
 ID AA011355 standard; Protein: 738 AA.  
 XX  
 AC AA011355;  
 XX  
 DT 26-MAR-2002 (first entry)  
 DE Human DNA cytokine receptor subunit 8 (DCRS8) polypeptide.  
 KW Human; DNA cytokine receptor subunit 8; DCRS8; phosphate labelling;  
 KW gene therapy; protein therapy; immunological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 25  
 FT /label- Val  
 FT /note- "Encoded by GTN"  
 XX  
 PN WO200190358-A2.  
 XX  
 PD  
 XX  
 PF 23-MAY-2001; 2001WO-US16767.  
 XX  
 PR 24-MAY-2000; 2000US-206862P.



XX (SCHE) SCHERING CORP.  
 XX Gorman DM;  
 XX WPI: 2002-106198/14.  
 DR N-PSDB; AAS18134.  
 XX Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders -  
 XX Claim 1; Page 25; 148pp; English.  
 XX The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRS8 polypeptide.  
 XX Sequence 738 AA;

Query Match 100.0%; Score 2210; DB 23; Length 738;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-210;  
 Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RKQOENYSHLDESSSTYTAALPRRLPRKPVLCYSSKQGNMNVVQCFAYFL 60  
 DB 321 RKQOENYSHLDESSSTYTAALPRRLPRKPVLCYSSKQGNMNVVQCFAYFL 380  
 QY 61 QDFGCEVALDMEDFSCRGQREWIQIHESQFIIVVCSKGMKYFDKRNKRGKG 120  
 DB 381 QDFGCEVALDMEDFSCRGQREWIQIHESQFIIVVCSKGMKYFDKRNKRGKG 440  
 QY 121 RSGKGELFVAVSATAELKROAKQSSAALSFAVTFDYSCGDVPGILDLSTKYL 180  
 DB 441 RSGKGELFVAVSATAELKROAKQSSAALSFAVTFDYSCGDVPGILDLSTKYL 500  
 QY 181 DNLPLCASHLSRDHGLQEPGQHTROGSRNYSKGRSLYVAICNMHGFIDEEDPWE 240  
 DB 501 DNLPLCASHLSRDHGLQEPGQHTROGSRNYSKGRSLYVAICNMHGFIDEEDPWE 560  
 QY 241 KQVFPFPPPLRYREPLVLEKDSGLVNDVNCXKPESDPGLKVAAYLVGATGPDSD 300  
 DB 561 KQVFPFPPPLRYREPLVLEKDSGLVNDVNCXKPESDPGLKVAAYLVGATGPDSD 620  
 QY 301 SOHGLDQDEARPDGSAALQPLHTVYAGSPDMPROSGIYDSSVPSSELSLPLMEG 360  
 DB 621 SOHGLDQDEARPDGSAALQPLHTVYAGSPDMPROSGIYDSSVPSSELSLPLMEG 680  
 QY 361 LSTDQETSLTESVSSSGLGEPEPPALPSKLLSSGSKADLCRSYTDLEHVAAPL 418  
 DB 681 LSTDQETSLTESVSSSGLGEPEPPALPSKLLSSGSKADLCRSYTDLEHVAAPL 738

RESULT 3  
 ANU10602  
 ID ANU10602 standard; Protein; 739 AA.  
 AC ANU10602;  
 XX (first entry)

XX Human Interleukin 17 (IL-17) receptor-like protein version 2.

KW Interleukin 17; IL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatitis; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; cachexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human.  
 XX Homo sapiens.  
 XX WO200168859-A2.  
 XX 20-SEP-2001.  
 XX 15-MAR-2001; 2001WO-US08678.  
 XX 16-MAR-2000; 2000US-189816P.  
 XX 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.  
 XX Jing S;  
 XX WPI: 2001-611392/70.  
 DR N-PSDB; AAS16201.  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,  
 XX diabetes, psoriasis and glaucoma.  
 XX Claim 2; Fig 1; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor-like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17r) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis), cancers (e.g. leukaemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17r may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17r antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of human Interleukin 17 (IL-17) receptor like protein described in the method of the invention.  
 CC Note: Residues 1-288 of this sequence correspond to residues 8-296 of the sequence shown in AAU10601 which is incomplete in the specification.

XX Sequence 739 AA;  
 Query Match 100.0%; Score 2210; DB 22; Length 739;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-210;  
 Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RKQOENYSHLDESSSTYTAALPRRLPRKPVLCYSSKQGNMNVVQCFAYFL 60  
 DB 322 RKQOENYSHLDESSSTYTAALPRRLPRKPVLCYSSKQGNMNVVQCFAYFL 381

QY 61 QDPCGEVALDWDPSLCRSGREWIQIHEISOFLIVVCSKGNKYFVDKKNYKHGGG 120  
 DB 382 QDPCGEVALDWDPSLCRSGREWIQIHEISOFLIVVCSKGNKYFVDKKNYKHGGG 441  
 QY 121 RSGSGELFVAVSAIAEKLRQAKSSAALSKFIATYDFYSCGDVPGILDSTKYRLM 180  
 DB 442 RSGSGELFVAVSAIAEKLRQAKSSAALSKFIATYDFYSCGDVPGILDSTKYRLM 501  
 QY 181 DNLPLQCSLHSDRDLQEPQGTROGSRNRYFRSKSGSLVAICNNHOFIDEEPWF 240  
 DB 502 DNLPLQCSLHSDRDLQEPQGTROGSRNRYFRSKSGSLVAICNNHOFIDEEPWF 561  
 QY 241 KQFVPPHPPPLRYEPVLEKFDGLVNDVCMKPGPESDCLKVEAAVLGATGPAISOHE 300  
 DB 562 KQFVPPHPPPLRYEPVLEKFDGLVNDVCMKPGPESDCLKVEAAVLGATGPAISOHE 621  
 QY 301 SOHGGDQDGEARALDGSAAALQPLLTHTVKAAGSPDMRDSGIYDSSVPSSELSPLMGG 360  
 DB 622 SOHGGDQDGEARALDGSAAALQPLLTHTVKAAGSPDMRDSGIYDSSVPSSELSPLMGG 681  
 QY 361 LSTDTQETSSLSSTSSVSSSGLGEEPPALPSKLLSSGCKADLCGRSTYDELHVAAPL 418  
 DB 682 LSTDTQETSSLSSTSSVSSSGLGEEPPALPSKLLSSGCKADLCGRSTYDELHVAAPL 739

## RESULT 4

ABB07628  
 ID ABB07628 standard; Protein: 739 AA.

AC ABB07628;

DT 2003-05-20 (first entry)

DE Human cytokine receptor, zcytor18 splice variant.

KW Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

OS Homo sapiens.

PN W0200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

PX (ZYMO ) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

DR WPI; 2002-217048/27.

DR N-PSDB; ABA95035, ABA95036.

FT New cytokine receptor polypeptide designated zcytor18, useful for  
 inhibiting cell proliferation associated with psoriasis or tumor  
 growth, and modulating immune system by binding to endogenous zcytor18  
 ligand

PS Claim 1; Page 102-106; 119pp; English.

CC The invention relates to an isolated cytokine receptor polypeptide  
 designated zcytor18. The zcytor18 polypeptides can be expressed by  
 standard recombinant methodology. The polypeptides can be used to inhibit  
 cell proliferation associated with psoriasis or tumour growth. The  
 encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 and localize zcytor18 gene expression in tissue samples. The probes are  
 also useful for detecting gross aberrations in chromosome 3 in which  
 zcytor18 gene resides. The zcytor18 polynucleotides can also be used in

CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 splice variant.

SQ Sequence 739 AA;

Query Match 100.0%; Score 2210; DB 23; Length 739;

Best Local Similarity 100.0%; Pred. No. 1.8e-210;

Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKQOENYISLHSDRDLQEPQGTROGSRNRYFRSKSGSLVAICNNHOFIDEEPWF 60

DB 322 RKQOENYISLHSDRDLQEPQGTROGSRNRYFRSKSGSLVAICNNHOFIDEEPWF 381

QY 61 QDPCGEVALDWDPSLCRSGREWIQIHEISOFLIVVCSKGNKYFVDKKNYKHGGG 120

DB 382 QDPCGEVALDWDPSLCRSGREWIQIHEISOFLIVVCSKGNKYFVDKKNYKHGGG 441

QY 121 RSGSGELFVAVSAIAEKLRQAKSSAALSKFIATYDFYSCGDVPGILDSTKYRLM 180

DB 442 RSGSGELFVAVSAIAEKLRQAKSSAALSKFIATYDFYSCGDVPGILDSTKYRLM 501

QY 181 DNLPLQCSLHSDRDLQEPQGTROGSRNRYFRSKSGSLVAICNNHOFIDEEPWF 240

DB 502 DNLPLQCSLHSDRDLQEPQGTROGSRNRYFRSKSGSLVAICNNHOFIDEEPWF 561

QY 241 KQFVPPHPPPLRYEPVLEKFDGLVNDVCMKPGPESDCLKVEAAVLGATGPAISOHE 300

DB 562 KQFVPPHPPPLRYEPVLEKFDGLVNDVCMKPGPESDCLKVEAAVLGATGPAISOHE 621

QY 301 SOHGGDQDGEARALDGSAAALQPLLTHTVKAAGSPDMRDSGIYDSSVPSSELSPLMGG 360

DB 622 SOHGGDQDGEARALDGSAAALQPLLTHTVKAAGSPDMRDSGIYDSSVPSSELSPLMGG 681

QY 361 LSTDTQETSSLSSTSSVSSSGLGEEPPALPSKLLSSGCKADLCGRSTYDELHVAAPL 418

DB 682 LSTDTQETSSLSSTSSVSSSGLGEEPPALPSKLLSSGCKADLCGRSTYDELHVAAPL 739

## RESULT 5

ABB07626  
 ID ABB07626 standard; Protein: 753 AA.

AC ABB07626;

DT 2003-05-20 (first entry)

DE Human cytokine receptor, zcytor18 amino acid sequence.

KW Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 KW erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

PN W0200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

PX (ZYMO ) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

DR WPI; 2002-217048/27.

DR N-PSDB; ABA95031, ABA95032.

FT New cytokine receptor polypeptide designated zcytor18, useful for  
 inhibiting cell proliferation associated with psoriasis or tumor

PT growth, and modulating immune system by binding to endogenous zcytor18  
 PT ligand.  
 XX claim 1; Page 2; 119pp; English.  
 XX The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumour growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 amino acid sequence.  
 XX Sequence 753 AA;

Query Match 100.0%; Score 2210; DB 23; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-210;  
 Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKQQENYSHLDESSSTYTAALPRERLPRPKVFLCTSSKQGNMNVVOCFAFYL 60  
 Db 336 RKQQENYSHLDESSSTYTAALPRERLPRPKVFLCTSSKQGNMNVVOCFAFYL 395  
 QY 61 QDFCGCEVALDLWEDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 120  
 Db 396 QDFCGCEVALDLWEDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 455  
 QY 121 RGSCKGELFLVAVSAIAEKLQAKQSSAALSKEPIANTFYDSCGDPGILDLSTKRYLM 180  
 Db 456 RGSCKGELFLVAVSAIAEKLQAKQSSAALSKEPIANTFYDSCGDPGILDLSTKRYLM 515  
 QY 181 DNLQCLSHLSHSDGLOEQHTRGSRNFRSKGRSLYVAICNMHQFIDEPEWFE 240  
 Db 516 DNLQCLSHLSHSDGLOEQHTRGSRNFRSKGRSLYVAICNMHQFIDEPEWFE 575  
 QY 241 KQFVPPHPPPLRYEPVLEKDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 300  
 Db 576 KQFVPPHPPPLRYEPVLEKDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 635  
 QY 301 SQHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRPSGIYDSSVPSSELSLPLMEG 360  
 Db 636 SQHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRPSGIYDSSVPSSELSLPLMEG 695  
 QY 361 LSTQDQETSLTESVSSSGGEGEPPALPSKLLSSGSCADIGCRSYTDELHVAVPL 418  
 Db 696 LSTQDQETSLTESVSSSGGEGEPPALPSKLLSSGSCADIGCRSYTDELHVAVPL 753

RESULT 6  
 ABB07627  
 ID ABB07627 standard; Protein; 753 AA.  
 XX ABB07627;  
 XX 20-MAY-2002 (first entry)  
 XX Human cytokine receptor, zcytor18 variant sequence.  
 DE Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;  
 KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 FH Misc-difference 269

FT /label= T269M  
 FT /note= "wild-type Thr is replaced with Met"  
 FT Misc-difference 750  
 FT /label= V750A  
 FT /note= "wild-type Val is replaced with Ala"  
 XX WO200208259-A2.  
 XX 23-JUL-2001; 2001WO-US23253.  
 XX 26-JUL-2000; 2000US-220747P.  
 XX (ZIMO ) ZYMOGENETICS INC.  
 XX Presnell SR, Kuestner RE, Gao Z;  
 XX WPI: 2002-217048/77;  
 XX N-PSDB; ABA95033; ABA95034.  
 XX New cytokine receptor polypeptide designated zcytor18, useful for  
 PT inhibiting cell proliferation associated with psoriasis or tumor  
 PT growth, and modulating immune system by binding to endogenous zcytor18.  
 PT ligand.  
 XX Disclosure; Page 94-98; 119pp; English.  
 XX The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumour growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 variant amino acid sequence.  
 XX Sequence 753 AA;

Query Match 99.8%; Score 2206; DB 23; Length 753;  
 Best Local Similarity 99.8%; Pred. No. 4.5e-210;  
 Matches 417; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RKQQENYSHLDESSSTYTAALPRERLPRPKVFLCTSSKQGNMNVVOCFAFYL 60  
 Db 336 RKQQENYSHLDESSSTYTAALPRERLPRPKVFLCTSSKQGNMNVVOCFAFYL 395  
 QY 61 QDFCGCEVALDLWEDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 120  
 Db 396 QDFCGCEVALDLWEDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 455  
 QY 121 RGSCKGELFLVAVSAIAEKLQAKQSSAALSKEPIANTFYDSCGDPGILDLSTKRYLM 180  
 Db 456 RGSCKGELFLVAVSAIAEKLQAKQSSAALSKEPIANTFYDSCGDPGILDLSTKRYLM 515  
 QY 181 DNLQCLSHLSHSDGLOEQHTRGSRNFRSKGRSLYVAICNMHQFIDEPEWFE 240  
 Db 516 DNLQCLSHLSHSDGLOEQHTRGSRNFRSKGRSLYVAICNMHQFIDEPEWFE 575  
 QY 241 KQFVPPHPPPLRYEPVLEKDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 300  
 Db 576 KQFVPPHPPPLRYEPVLEKDFSLCRGQREWVQIKIHESQFIIVVCSKGMKIFVDRKNTKHKGGG 635  
 QY 301 SQHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRPSGIYDSSVPSSELSLPLMEG 360  
 Db 636 SQHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRPSGIYDSSVPSSELSLPLMEG 695

QY 361 LSTDTSTSLTSSVSSGLGEEPPALPSKLLSSGSKADLCGRSTYDELHVAAPL 418  
DB 696 LSTDTSTSLTSSVSSGLGEEPPALPSKLLSSGSKADLCGRSTYDELHVAAPL 753

RESULT 7  
AAU09904 standard; Protein: 738 AA.

AC AAU09904;  
DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein.

Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
bone disease; vascular disorder; eye disorder; cancer; human.

OS Homo sapiens.

XX WO200168859-A2

PN 2001-01-01

PD 2001-01-01

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

PR 28-NOV-2000; 2000US-0724460.

XX (ANGE-) AMGEN INC.

XX Jing S;

XX WPI: 2001-611392/70.

DR N-PSDB; AAS15346.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
diabetes, psoriasis and glaucoma.

XX Claim 2; Page 152-154; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
receptor like polypeptides useful as vaccines and in gene therapy. These  
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
ophthalmological activities. The IL-17 receptor like nucleic acids and  
proteins may be used to prevent and treat diseases associated with  
inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
include, for example immune disorders (e.g. inflammation, diabetes and  
transplant rejection), infections (e.g. hepatitis and septicemia),  
weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
(e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
breast cancer), reproductive disorders (e.g. infertility and  
miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
DNA and its complements may also be used as diagnostic probes to detect and  
quantitate the presence of similar nucleic acids in samples and identify  
patients needing restorative therapy. The IL17rlp may also be used as  
antigens in the production of antibodies against the proteins and in  
assays to identify modulators of expression and activity. The  
anti-IL17rlp antibodies and antagonists may also be used to down regulate  
expression and activity. This is the amino acid sequence of the human

CC Interleukin 17 (IL-17) receptor like protein described in the method of  
the invention.  
XX Sequence - 738 AA;

Query Match 99.68; Score 2201; DB:22; Length: 738;  
Best Local Similarity 99.88; Pred. No. 146-209;  
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKQOENIYSHLDSESSSTYTAALPRRLPRKVFVLYCYSSKDSQGNHNVVQCFAIFL 60  
DB 322 RKQOENIYSHLDSESSSTYTAALPRRLPRKVFVLYCYSSKDSQGNHNVVQCFAIFL 381  
QY 61 QDFCGEVALDLWEDFSLCREGQREWYQIKIHESQFIIVVCSKGMKIFVYDKNKKHKG 120  
DB 382 QDFCGEVALDLWEDFSLCREGQREWYQIKIHESQFIIVVCSKGMKIFVYDKNKKHKG 441  
QY 121 RGSCKGELFVAVSAIAEKLRQKSSAALSKEFLAVFYDSCGDPVGLDLSKYRLM 180  
DB 442 RGSCKGELFVAVSAIAEKLRQKSSAALSKEFLAVFYDSCGDPVGLDLSKYRLM 501  
QY 181 DNLPLCSLHLSRDLGELCPQHTROGSRNTFRSKGSLTVAICNMHQTDEPDWFE 240  
DB 502 DNLPLCSLHLSRDLGELCPQHTROGSRNTFRSKGSLTVAICNMHQTDEPDWFE 561  
QY 241 KQVFPFPPPLRYREPVLKEDSGVLVNDVWCKPGPESDFCLKVEAVLGTGTPADSOHE 300  
DB 562 KQVFPFPPPLRYREPVLKEDSGVLVNDVWCKPGPESDFCLKVEAVLGTGTPADSOHE 621  
QY 301 SQHGLDQDGEARPALDGSAAALPILHTVAGSPDMPDPSGDIYDSVTSSELSLPIMEG 360  
DB 622 SQHGLDQDGEARPALDGSAAALPILHTVAGSPDMPDPSGDIYDSVTSSELSLPIMEG 681  
QY 361 LSTDQTTSLTSSVSSGLGEEPPALPSKLLSSGSKADLCGRSTYDELHVAAP 417  
DB 682 LSTDQTTSLTSSVSSGLGEEPPALPSKLLSSGSKADLCGRSTYDELHVAAP 738

RESULT 8  
AAU09951 standard; Protein: 738 AA.

AC AAU09951;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein-substitution #1.  
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
mucin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 45 /label- Gly, Pro or Ala

XX WO200168859-A2

XX 20-SEP-2001

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX

PA (AMGE-) ANGEN INC.  
XX Jing S;  
XX WPI: 2001-611392/70.  
XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma -  
XX Claim 18; Page -: 158pp; English.  
XX The invention describes novel nucleic acids encoding Interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantify the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17r may also be used as  
XX Note: This sequence is not given in the specification but is based on the  
XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
XX and has been created according to information given in claim 18.  
XX Sequence 738 AA:  
Query Match 99.6%; Score 2201; DB 22; Length 738;  
Best Local Similarity 99.8%; Pred. No. 1.4e-209;  
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RKQENIYSHLDESESTYPAALPRERLPKPVFLCYSSKQGNHNVVQCFAYFL 60  
DB 322 RKQENIYSHLDESESTYPAALPRERLPKPVFLCYSSKQGNHNVVQCFAYFL 381  
QY 61 QDPCGCEVALDWEFSLCREGREWIQKHESOFIIVVCSSKGMFYDKNNKRGKG 120  
DB 382 QDPCGCEVALDWEFSLCREGREWIQKHESOFIIVVCSSKGMFYDKNNKRGKG 441  
QY 121 RSGSGEFLVAVSAIAEKLRQAKQSSAALSKEIATVDFYSCGDPVCPILDLSTKYLRL 180  
DB 442 RSGSGEFLVAVSAIAEKLRQAKQSSAALSKEIATVDFYSCGDPVCPILDLSTKYLRL 501  
QY 191 DNLPLCSLHLSRDRHGLQEPQTRGSRNRYFSGRSILYVAINCMHOFIDEEPWFE 240  
DB 502 DNLPLCSLHLSRDRHGLQEPQTRGSRNRYFSGRSILYVAINCMHOFIDEEPWFE 561  
QY 241 KQVFPHPPLRYEPFLVLEKFDGLVNDVCKPGPDSDFCLKVEAVLGATGPAQDSQHE 300  
DB 562 KQVFPHPPLRYEPFLVLEKFDGLVNDVCKPGPDSDFCLKVEAVLGATGPAQDSQHE 621  
QY 301 SQHGGGLQDGEARPAIDGSAALQPLRTYKAGSPDMPROSGDYSDSVPSSELSPLNMEG 360  
DB 622 SQHGGGLQDGEARPAIDGSAALQPLRTYKAGSPDMPROSGDYSDSVPSSELSPLNMEG 681  
QY 361 LSTDQTFSTSLTESVSSSGIGEEPPALPSKLLSSGCKADLCGRSYTDELHNAVAP 417

DB 582 LSTDQTFSTSLTESVSSSGIGEEPPALPSKLLSSGCKADLCGRSYTDELHNAVAP 738  
RESULT 9  
AAU09952  
ID AAU09952 standard; Protein, 738 AA.  
XX AC AAU09952;  
XX 14-FEB-2002 (first entry)  
XX Human Interleukin 17 (hIL-17) receptor like protein substitution #2.  
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
XX osteopathic; vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
XX mutein.  
XX Homo sapiens.  
XX OS Synthetic.  
XX Key Location/Qualifiers  
XX Misc-difference 227 /label= Phe, Leu, Val, Ile, Ala, Tyr  
XX WC200168859-A2  
XX 15-MAR-2001; 2001MO-0508678.  
XX 16-MAR-2000; 2000US-189816P.  
XX 28-NOV-2000; 2000US-0724460.  
XX (AMGE-) ANGEN INC.  
XX Jing S;  
XX WPI: 2001-611392/70.  
XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma -  
XX Claim 19; Page -: 158pp; English.  
XX The invention describes novel nucleic acids encoding Interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantify the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17r may also be used as

CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17 receptor-like polypeptides and antagonists may also be used to down-regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human interleukin 17 (IL-17) receptor like protein sequence (AA009904)  
 CC and has been created according to information given in claim 19.  
 XX  
 XX

XX Sequence 738 AA;

Query Match 99.6%; Score 2201; DB 22; Length 738;  
 Best Local Similarity 99.8%; Pred. No. 1.4e-209;  
 Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKQCEYTHLDESSSTYTAALPRRLPRKPVFLCSKDGQNNHNVQCFAYFL 60  
 DB 322 RKQCEYTHLDESSSTYTAALPRRLPRKPVFLCSKDGQNNHNVQCFAYFL 381  
 QY 61 QDFCCGCEVALDMEFSLCRGQEWYQIKIHESQFIIVVCSKGMKFFVDKKNYKKG 120  
 DB 382 QDFCCGCEVALDMEFSLCRGQEWYQIKIHESQFIIVVCSKGMKFFVDKKNYKKG 441  
 QY 121 RSGSGELFLVAVSAIAEKLRQAKQSSAALSFKFTANTFYDSCGDVPGILDLSTKRLM 180  
 DB 442 RSGSGELFLVAVSAIAEKLRQAKQSSAALSFKFTANTFYDSCGDVPGILDLSTKRLM 501  
 QY 181 DNLPLCSHLRSHDGLQPGQRTQGRNRYFRSKGSLYVAICNMHOFIDEEPWF 240  
 DB 502 DNLPLCSHLRSHDGLQPGQRTQGRNRYFRSKGSLYVAICNMHOFIDEEPWF 561  
 QY 241 KQVFPHPPPLRYREPVLKFDGLVNDVCKPGPESDFCLAYEAVPLGATGADPSQHE 300  
 DB 562 KQVFPHPPPLRYREPVLKFDGLVNDVCKPGPESDFCLAYEAVPLGATGADPSQHE 621  
 QY 301 SQRGGLDQGEARPDALDGAALQPLHRTVAGSPDMRDSGIYDSSVPSSELPLMG 360  
 DB 622 SQRGGLDQGEARPDALDGAALQPLHRTVAGSPDMRDSGIYDSSVPSSELPLMG 681  
 QY 361 LSTDTQTSSTTSVSSSGIGEREPPALPSKLLSSGCKADLCRSTYTDLHNAV 417  
 DB 682 LSTDTQTSSTTSVSSSGIGEREPPALPSKLLSSGCKADLCRSTYTDLHNAV 738

RESULT 10  
 AA009953  
 ID AA009953 standard; Protein; 738 AA.

XX AA009953;

XX 14-~~15~~ First entry)

XX Human interleukin 17 (IL-17) receptor like protein substitution #3.

XX Interleukin 17; IL-17 receptor like protein; immunomodulatory;  
 XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 XX vascular; cycostatic; anti-leukemic; anti-infertility; ophthalmological;  
 XX hepatitis; cachexia; cachexia; neuronal dysfunction; lung disease;  
 XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 XX muteln.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 363

XX /label= Ser, Thr, Ala, Cys

XX W0200168859-A2.

XX 20-SEP-2001.

XX

PF 15-MAR-2001; 2001WO-08678  
 XX  
 PR 16-MAR-2000; 2000US-189816P  
 PR 28-NOV-2000; 2000US-074460  
 XX  
 PA (AMCE)- AMGEN INC.  
 XX  
 PI Jing S;  
 XX  
 DR WPI; 2001-611392/70.  
 XX  
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX  
 PS Claim 20; Page 158pp; English.  
 XX

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, and  
 XX osteopathic, vascular, cycostatic, anti-leukemic, anti-infertility and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (IL17p) expression. These  
 XX include, for example immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infections (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of similar nucleic acids in samples and identify  
 XX patients needing restorative therapy. The IL17p may also be used as  
 XX antigens in the production of antibodies against the proteins and in  
 XX assays to identify modulators of expression and activity. This  
 XX anti-IL17p antibodies and antagonists may also be used to down regulate  
 XX expression and activity.  
 XX Note: This sequence is not given in the specification but is based on the  
 XX human interleukin 17 (IL-17) receptor like protein sequence (AA009904)  
 XX and has been created according to information given in claim 20.

XX Sequence 738 AA;

Query Match 99.4%;

Best Local Similarity 99.5%; Pred. No. 3.4e-209;

Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKQCEYTHLDESSSTYTAALPRRLPRKPVFLCSKDGQNNHNVQCFAYFL 60  
 DB 322 RKQCEYTHLDESSSTYTAALPRRLPRKPVFLCSKDGQNNHNVQCFAYFL 381  
 QY 61 QDFCCGCEVALDMEFSLCRGQEWYQIKIHESQFIIVVCSKGMKFFVDKKNYKKG 120  
 DB 382 QDFCCGCEVALDMEFSLCRGQEWYQIKIHESQFIIVVCSKGMKFFVDKKNYKKG 441  
 QY 121 RSGSGELFLVAVSAIAEKLRQAKQSSAALSFKFTANTFYDSCGDVPGILDLSTKRLM 180  
 DB 442 RSGSGELFLVAVSAIAEKLRQAKQSSAALSFKFTANTFYDSCGDVPGILDLSTKRLM 501  
 QY 181 DNLPLCSHLRSHDGLQPGQRTQGRNRYFRSKGSLYVAICNMHOFIDEEPWF 240  
 DB 502 DNLPLCSHLRSHDGLQPGQRTQGRNRYFRSKGSLYVAICNMHOFIDEEPWF 561  
 QY 241 KQVFPHPPPLRYREPVLKFDGLVNDVCKPGPESDFCLAYEAVPLGATGADPSQHE 300  
 DB 562 KQVFPHPPPLRYREPVLKFDGLVNDVCKPGPESDFCLAYEAVPLGATGADPSQHE 621



CC 301 SQGGGLDQGEARPAIDGSAALQPLHTVKAQSPDMRDSGIYDSSVPSSELSPLMEG 360  
CC 622 SQGGGLDQGEARPAIDGSAALQPLHTVKAQSPDMRDSGIYDSSVPSSELSPLMEG 681  
CC 361 LSTDDTETSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLGCSTYDELHAPV 417  
CC 682 LSTDDTETSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLGCSTYDELHAPV 738

RESULT 11  
AAU09954  
ID AAU09954 standard; Protein; 738 AA.

XX AC AAU09954;  
XX 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #4.  
KW Interleukin-17; hIL-17 receptor like protein; immunomodulatory;  
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
KW mutin.  
XX Homo sapiens.  
OS Synthetic.

XX Key Location/Qualifiers  
XX Misc-difference 374 /label= Val, Ile, Met, Leu, Phe, Ala, Nle.

XX WO200168859-A2.  
XX 15-MAR-2001; 2001WO-US08678.  
XX 16-MAR-2000; 2000US-189846P.  
XX 28-NOV-2000; 2000US-072460.  
XX (AMGE-) AMGEN INC.  
XX Jing S;  
XX WPI; 2001-611392/70.

XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma.  
XX Claim 21; Page -; 158pp; English.

XX The invention describes novel nucleic acids encoding Interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17R) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and

CC breast cancer), reproductive disorders (e.g. infertility and  
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
CC DNA and its complements may also be used as diagnostic probes to detect and  
CC quantitate the presence of similar nucleic acids in samples and identify  
CC patients needing restorative therapy. The IL17R may also be used as  
CC antigens in the production of antibodies against the proteins and in  
CC assays to identify modulators of expression and activity. The  
CC anti-IL17R antibodies and antagonists may also be used to down regulate  
CC expression and activity.  
CC Note: This sequence is not given in the specification but is based on the  
CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904),  
CC and has been created according to information given in claim 21.

XX Sequence 738 AA;  
Query Match 99.43; Score 2196; DB 22; Length 738;  
Best Local Similarity 99.5%; Pred. No. 4.3e-205;  
Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKQQENYSHLDESESTTAALPRERLRPRKPVFLCYSSKDGQNHNVVOCFAYEL 60  
DB 322 RKQQENYSHLDESESTTAALPRERLRPRKPVFLCYSSKDGQNHNVVOCFAYEL 381  
QY 61 QDFCCEVALDLNEDFSLCREGREWIQKTHESQFIIVVCSKGMKTFYDKNKRKGGG 120  
DB 382 QDFCCEVALDLNEDFSLCREGREWIQKTHESQFIIVVCSKGMKTFYDKNKRKGGG 441  
QY 121 RGSKGELFLVAVSAEKLRAKQSSAALSFIATVFDYSCGDVPGILDLSYRLM 180  
DB 442 RGSKGELFLVAVSAEKLRAKQSSAALSFIATVFDYSCGDVPGILDLSYRLM 501  
QY 181 DNLPLCSHLSRHGLOEPGORTGSRNRYFSKSGSLAVACNMHOFIDEEDPWE 240  
DB 502 DNLPLCSHLSRHGLOEPGORTGSRNRYFSKSGSLAVACNMHOFIDEEDPWE 561  
QY 241 KQVFPFPPPLRYEPVLEKFSGLVNDVNCCKPESDFCLKVEAVLAVGATGPDQSHE 300  
DB 562 KQVFPFPPPLRYEPVLEKFSGLVNDVNCCKPESDFCLKVEAVLAVGATGPDQSHE 621  
QY 301 SQGGGLDQGEARPAIDGSAALQPLHTVKAQSPDMRDSGIYDSSVPSSELSPLMEG 360  
DB 622 SQGGGLDQGEARPAIDGSAALQPLHTVKAQSPDMRDSGIYDSSVPSSELSPLMEG 681  
QY 361 LSTDDTETSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLGCSTYDELHAPV 417  
DB 682 LSTDDTETSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLGCSTYDELHAPV 738

RESULT 12  
AAU09956  
ID AAU09956 standard; Protein; 738 AA.

XX AC AAU09956;  
XX 14-FEB-2002 (first entry)

DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.  
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
KW mutin.  
XX Homo sapiens.  
OS Synthetic.

XX Key Location/Qualifiers  
XX Misc-difference 515 /label= Asp, Glu

XX WO200168859-A2  
XX 20-SEP-2001.  
XX 15-MAR-2001; 2001WO-US08678.  
XX 16-MAR-2000; 2000US-189816P.  
XX 28-NOV-2000; 2000US-0724460.  
XX (AMGE-) AMGEN INC.  
XX Jing S;  
XX WPI; 2001-611392/70.  
XX Nucleic acids encoding interleukin 17 receptor like polypeptides.  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma.  
XX Claim 23; Page -: 158pp; English.  
XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
XX bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
XX breast cancer), reproductive disorders (e.g. infertility and  
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
XX DNA and its complements may also be used as diagnostic probes to detect and  
XX quantitate the presence of similar nucleic acids in samples and identify  
XX patients needing restorative therapy. The IL17rp may also be used as  
XX antigens in the production of antibodies against the proteins and in  
XX assays to identify modulators of expression and activity. The  
XX anti-IL17rp antibodies and antagonists may also be used to down regulate  
XX expression and activity.  
XX Note: This sequence is not given in the specification but is based on the  
XX human interleukin 17 (IL-17) receptor like protein sequence (AA09904)  
XX and has been created according to information given in claim 23.

XX Sequence 738 AA;  
XX Query Match 99.3%; Score 2194; DB 22; Length 738;  
XX Best Local Similarity 99.5%; Pred. No. 6.8e-209;  
XX Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX 1 RKQOENYSHLDESESTYTAALPRRLPRPVFLCYSSKDGQNNHVVQCFAYFL 60  
XX 322 RKQOENYSHLDESESTYTAALPRRLPRPVFLCYSSKDGQNNHVVQCFAYFL 381  
XX 61 QPCCCEVALDWDSESLCRESQEWVQIKHESQFIIVVCSKGMKVFVDKNNKKGGS 120  
XX 382 QPCCCEVALDWDSESLCRESQEWVQIKHESQFIIVVCSKGMKVFVDKNNKKGGS 441  
XX 121 RSGSGELFLVNSAETAKLRQAKOSSSALSKFIIVYDSCSDVPGILDISTYRLM 180  
XX 442 RSGSGELFLVNSAETAKLRQAKOSSSALSKFIIVYDSCSDVPGILDISTYRLM 501  
XX 181 DNLPLCSLHSHRDLQEPGQHTQSGRRNRYFRSKSGSLYVAICNNHQFIDEEPDPNE 240  
XX 502 DNLPLCSLHSHRDLQEPGQHTQSGRRNRYFRSKSGSLYVAICNNHQFIDEEPDPNE 561

XX 241 KQVPEPPPLRYREPVLKEDSGVLNDVNCIKGPPESDCLKVAAYLVGATGAPDSQHE 300  
XX 562 KQVPEPPPLRYREPVLKEDSGVLNDVNCIKGPPESDCLKVAAYLVGATGAPDSQHE 621  
XX 301 SOHGLDQGEARPALDGSAAIQPLLTWKAGSPDMPRDSGIYDSVPSSELSLPLMEG 360  
XX 622 SOHGLDQGEARPALDGSAAIQPLLTWKAGSPDMPRDSGIYDSVPSSELSLPLMEG 681  
XX 361 LSTQDTSTSLTESVSSSGIGEEPPALPFLKSSGCKADLGCRSYTDELHAYAP 417  
XX 682 LSTQDTSTSLTESVSSSGIGEEPPALPFLKSSGCKADLGCRSYTDELHAYAP 738  
XX RESULT 13  
XX AA09955  
XX ID AA09955 standard; Proteins: 738 AA.  
XX AC AA09955;  
XX DT 14-FEB-2002 (first entry)  
XX Human Interleukin 17 (hIL-17) receptor like protein substitution #5.  
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
XX vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
XX mitein.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX FT Misc-difference 385 /Label= Cys, Ser, Ala  
XX WO200168859-A2.  
XX 20-SEP-2001.  
XX 15-MAR-2001; 2001WO-US08678.  
XX 16-MAR-2000; 2000US-189816P.  
XX 28-NOV-2000; 2000US-0724460.  
XX (AMGE-) AMGEN INC.  
XX Jing S;  
XX WPI; 2001-611392/70.  
XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
XX diabetes, psoriasis and glaucoma.  
XX Claim 22; Page -: 158pp; English.  
XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
XX receptor like polypeptides useful as vaccines and in gene therapy. These  
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
XX proteins may be used to prevent and treat diseases associated with  
XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
XX include, for example immune disorders (e.g. inflammation, diabetes and  
XX transplant rejection), infections (e.g. hepatitis and septicemia),  
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal



CC dysfunction (e.g., Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g., cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g., eczema and psoriasis), kidney disease (e.g., glomerulonephritis),  
 CC bone diseases (e.g., osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g., stroke and atherosclerosis), cancers (e.g., leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g., infertility and  
 CC miscarriage), eye disorders (e.g., glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rlp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 24.  
 XX Sequence 738 AA;

Query Match 99.1%; Score 2190; DB 22; Length 738;  
 Best Local Similarity 99.5%; Pred. No. 1.7e-208;  
 Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RKQENIYSHLDEESSESTTAALPRRLPRPRKPVFLCYSSKDGQNNHNVQCPAYFL 60  
 DB 322 RKQENIYSHLDEESSESTTAALPRRLPRPRKPVFLCYSSKDGQNNHNVQCPAYFL 381  
 QY 61 QDFCGEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVCKNKHKGG 120  
 DB 382 QDFCGEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVCKNKHKGG 441  
 QY 121 RGSKGELFLVAVSAIAEKLRQAKSSAALSKFIATVYDCSDGVPGLDLSKYRLM 180  
 DB 442 RGSKGELFLVAVSAIAEKLRQAKSSAALSKFIATVYDCSDGVPGLDLSKYRLM 501  
 QY 181 DNLQCLSHLSRHDGLQEPQGTQGRNRNIFSKSGSLVAVICNHHOFIDEEPWF 240  
 DB 502 DNLQCLSHLSRHDGLQEPQGTQGRNRNIFSKSGSLVAVICNHHOFIDEEPWF 561  
 QY 241 KQVPFPHPPPLRYREPVLEKFDGLVNDVNCVKPGESDFCLKVAAPVIGATGPADSOE 300  
 DB 562 KQVPFPHPPPLRYREPVLEKFDGLVNDVNCVKPGESDFCLKVAAPVIGATGPADSOE 621  
 QY 301 SQHGGLDGGEARLQDGAALQPLHVTWKAGSPDMRPSDGLYDSSVPSSELPLMEG 360  
 DB 622 SQHGGLDGGEARLQDGAALQPLHVTWKAGSPDMRPSDGLYDSSVPSSELPLMEG 681  
 QY 361 LSTDQETSSLTSSVSSSGGEEPPALPSKLLSSCGKADLCRSTYDELHAPV 417  
 DB 682 LSTDQETSSLTSSVSSSGGEEPPALPSKLLSSCGKADLCRSTYDELHAPV 738

RESULT 14  
 AAU09957  
 ID AAU09957 standard; Protein; 738 AA.  
 XX AAU09957;  
 XX 14-FEB-2002 (first entry)  
 DT Human Interleukin 17 (IL-17) receptor like protein substitution #7.  
 DE Interleukin 17; IL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-Alzheimer's; anti-Parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutin.  
 XX Homo sapiens.

OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 602 /label- Cys, Ala, Ser  
 FT  
 XX  
 XX W0200168859-A2.  
 XX 20-SEP-2001.  
 XX  
 XX 15-MAR-2001; 2001WO-US08678.  
 XX  
 XX 16-MAR-2000; 2000US-189816P.  
 XX 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.  
 XX Jing S;  
 XX  
 XX MPI; 2001-611392/70.  
 XX  
 XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX diabetes, psoriasis and glaucoma  
 XX  
 XX Claim 24; Page -: 158pp; English.  
 XX  
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-Alzheimer's, renal,  
 XX anti-Parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 XX osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 XX include, for example immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infections (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of similar nucleic acids in samples and identify  
 XX patients needing restorative therapy. The IL17rlp may also be used as  
 XX antigens in the production of antibodies against the proteins and in  
 XX assays to identify modulators of expression and activity. The  
 XX anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 XX expression and activity.  
 XX Note: This sequence is not given in the specification but is based on the  
 XX human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 XX and has been created according to information given in claim 24.

Sequence 738 AA;  
 Query Match 99.1%; Score 2190; DB 22; Length 738;  
 Best Local Similarity 99.5%; Pred. No. 1.7e-208;  
 Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RKQENIYSHLDEESSESTTAALPRRLPRPRKPVFLCYSSKDGQNNHNVQCPAYFL 60  
 DB 322 RKQENIYSHLDEESSESTTAALPRRLPRPRKPVFLCYSSKDGQNNHNVQCPAYFL 381  
 QY 61 QDFCGEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVCKNKHKGG 120  
 DB 382 QDFCGEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVCKNKHKGG 441  
 QY 121 RGSKGELFLVAVSAIAEKLRQAKSSAALSKFIATVYDCSDGVPGLDLSKYRLM 180  
 DB 442 RGSKGELFLVAVSAIAEKLRQAKSSAALSKFIATVYDCSDGVPGLDLSKYRLM 501  
 QY 181 DNLQCLSHLSRHDGLQEPQGTQGRNRNIFSKSGSLVAVICNHHOFIDEEPWF 240  
 DB 502 DNLQCLSHLSRHDGLQEPQGTQGRNRNIFSKSGSLVAVICNHHOFIDEEPWF 561  
 QY 241 KQVPFPHPPPLRYREPVLEKFDGLVNDVNCVKPGESDFCLKVAAPVIGATGPADSOE 300  
 DB 562 KQVPFPHPPPLRYREPVLEKFDGLVNDVNCVKPGESDFCLKVAAPVIGATGPADSOE 621  
 QY 301 SQHGGLDGGEARLQDGAALQPLHVTWKAGSPDMRPSDGLYDSSVPSSELPLMEG 360  
 DB 622 SQHGGLDGGEARLQDGAALQPLHVTWKAGSPDMRPSDGLYDSSVPSSELPLMEG 681  
 QY 361 LSTDQETSSLTSSVSSSGGEEPPALPSKLLSSCGKADLCRSTYDELHAPV 417  
 DB 682 LSTDQETSSLTSSVSSSGGEEPPALPSKLLSSCGKADLCRSTYDELHAPV 738

Db 442 RSGKGLFLVAVSAIAEKLRQAKQSSAALSKFTAVTDFSCGDPVPCGILDLSTKYRLM 501  
 QY 181 DNLPOLCSHLSRDRGLQEPQRTGSRNTFRSKGSRISLYVAICNNHOFIDEEPWF 240  
 Db 502 DNLPOLCSHLSRDRGLQEPQRTGSRNTFRSKGSRISLYVAICNNHOFIDEEPWF 561  
 QY 241 KQVFFPPPLRTREPVLEKFDGSLVNDVCKPGPESDFCLKVEAVIYGATGPAQSOHE 300  
 Db 562 KQVFFPPPLRTREPVLEKFDGSLVNDVCKPGPESDFCLKVEAVIYGATGPAQSOHE 621  
 QY 301 SOHGLDQDGEARPDALDGSAAALQPLHTVKAGSPDMPRDGIYDSSVPSSELSLPLAEG 360  
 Db 622 SOHGLDQDGEARPDALDGSAAALQPLHTVKAGSPDMPRDGIYDSSVPSSELSLPLAEG 681  
 QY 361 LSTQDTETSSLTSSVSSSGLGEPEPPALPSKLLSSGCKDLGCRSYTDELHAPV 417  
 Db 682 LSTQDTETSSLTSSVSSSGLGEPEPPALPSKLLSSGCKDLGCRSYTDELHAPV 738

RESULT 15

ABB07630  
 ID ABB07630 standard; Protein; 739 AA.

XX AC ABB07630;

XX DT 09-MAY-2002 First entry

XX DE Murine cytokine receptor, zcytor18.

XX KW Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
 XX KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 XX KW erythroleukemia; chromosome 3p14.3; gene therapy; mouse.

XX OS Mus sp.

XX PN WO200208259-A2.

XX PD 31-JAN-2002.

XX PF 23-JUL-2001; 2001WO-US3233.

XX PR 26-JUL-2000; 2000US-220747P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, Kuestner RE, Gao Z;

XX PS WPI; 2002-217048/27.

XX DR N-PSDB; ABA95037, ABA95038.

XX PT New cytokine receptor polypeptide designated zcytor18, useful for  
 XX PT inhibiting cell proliferation associated with psoriasis or tumor  
 XX PT growth, and modulating immune system by binding to endogenous zcytor18  
 XX PT ligand

XX PS Claim 1: Page 111-115; 119pp; English.

XX CC The invention relates to an isolated cytokine receptor polypeptide  
 XX CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 XX CC standard recombinant methodology. The polypeptides can be used to inhibit  
 XX CC cell proliferation associated with psoriasis or tumor growth. The  
 XX CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 XX CC therapy techniques. zcytor18 oligonucleotide probes are useful for in  
 XX CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 XX CC and localize zcytor18 gene expression in tissue samples. The probes are  
 XX CC also useful for detecting gross aberrations in chromosome 3 in which  
 XX CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 XX CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 XX CC periodic fever, and erythroleukemia, and erythroleukemia associated with  
 XX CC polymorphisms of cytokine receptors. The present sequence represents a  
 XX CC murine zcytor18 amino acid sequence.

XX SQ Sequence 739 AA;

Query Match: 82.1% Score: 1813.5; DB: 23; Length: 739;  
 Best Local Similarity: 83.1%; Pred. No. 4; 9e-171;  
 Matches: 350; Conservative: 25; Mismatches: 39; Indels: 7; Gaps: 4;

QY 1 RKQKQNIYSHLDESSESSTTAALPRERLRPRKPVFLCYTSKQGNHNAVQCFAYFL 60  
 Db 332 RKQKQNIYSHLDESSESSTTAALPRERLRPRKPVFLCYTSKQGNHNAVQCFAYFL 382  
 QY 61 QDRCGCEVALDWEFSLCREGQREWIQKHESQFIIVVCSKGMKIFVKKKHKGG 120  
 Db 383 QDRCGCEVALDWEFSLCREGQREWIQKHESQFIIVVCSKGMKIFVKKKHKGG 442  
 QY 121 RGSCKGELELVAVSAIAEKLRQAKQSSAALSKFTAVTDFSCGDPVPCGILDLSTKYRLM 180  
 Db 443 RGSCKGELELVAVSAIAEKLRQAKQSSAALSKFTAVTDFSCGDPVPCGILDLSTKYRLM 502  
 QY 181 DNLPOLCSHLSRDRGLQEPQRTGSRNTFRSKGSRISLYVAICNNHOFIDEEPWF 239  
 Db 503 DNLPOLCSHLSRDRGLQEPQRTGSRNTFRSKGSRISLYVAICNNHOFIDEEPWF 559  
 QY 240 KQVFFPPPLRTREPVLEKFDGSLVNDVCKPGPESDFCLKVEAVIYGATGPAQSOH 299  
 Db 560 KQVFFPPPLRTREPVLEKFDGSLVNDVCKPGPESDFCLKVEAVIYGATGPAQSYS 619  
 QY 300 --ESQSGGLDQDGEARPDALDGSAAALQPLHTVKAGSPDMPRDGIYDSSVPSSELSLPL 357  
 Db 620 YLESQHVGLDQDTEAQPSCDAPALQPLHTVKAGSPDMPRDGIYDSSVPSSELSLPL 679  
 QY 358 MEGLSLDQETSLTESVSSSGLGEPEPPALPSKLLSSGCKDLGCRSYTDELHAPV 417  
 Db 680 MEGLSLDQETSLTESVSSSGLGEPEPPALPSKLLSSGCKDLGCRSYTDELHAPV 738  
 QY 418 L 418  
 Db 739 L 739

Search completed: May 19, 2003, 09:20:02  
 Job time: 32.4416 secs

GenCore version 5.1.4.p5.4578  
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QM protein - protein search, using sw model

Run on: May 19, 2003, 09:08:53 ; Search time 8.48731 Seconds  
(without alignments)  
2042.709 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_336\_753

Perfect score: 2210

Sequence: 1 RKQOENYSHLDESSSS .....CFADLGCRSYDELHNAVPL 418

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	308	13.9	866	1	Q96f46 homo sapien
2	289.5	13.1	864	1	Q60943 mus musculus
3	127.5	5.8	502	1	Q9arm6 homo sapien
4	126	5.7	718	1	Q91028 caenorhabdi
5	110.5	5.0	499	1	Q911p3 mus musculus
6	105.5	4.8	592	1	Q60770 mus musculus
7	99.5	4.5	794	1	Q60821 mus musculus
8	96.5	4.4	746	1	P04521 abelson: mur
9	96	4.3	660	1	Q04996 arabidopsis
10	95	4.3	933	1	P08401 homo sapien
11	94.5	4.3	841	1	Q69154 murine cyto
12	93.5	4.2	806	1	Q04982 gallus gall
13	93.5	4.2	807	1	P34908 coturnix co
14	92.5	4.2	347	1	Q62421 mus musculus
15	92.5	4.2	548	1	P98154 mus musculus
16	92.5	4.2	830	1	Q96r59 mus musculus
17	92.5	4.2	2314	1	P23471 homo sapien
18	92	4.2	864	1	Q02799 sus scrofa
19	92	4.2	883	1	Q61361 mus musculus
20	91.5	4.1	351	1	P20271 caenorhabdi
21	91	4.1	883	1	P55068 rattus norv
22	91	4.1	2038	1	P13709 drosophila
23	90.5	4.1	895	1	Q97952 macaca fasc
24	90	4.1	579	1	P13080 aedes aegypt
25	90	4.1	803	1	Q13105 homo sapien
26	89.5	4.0	766	1	P36085 saccaromyc
27	88.5	4.0	797	1	Q9b900 homo sapien
28	88.5	4.0	1992	1	Q14669 homo sapien
29	88.5	4.0	2273	1	Q95180: homo sapien
30	88	4.0	229	1	P06425 human papill
31	88	4.0	638	1	P05652 bacillus su
32	88	4.0	770	1	Q62440 mus musculus
33	88	4.0	782	1	Q35218 mus musculus

#### ALIGNMENTS

##### RESULT 1

IL17R\_HUMAN  
ID IL17R\_HUMAN STANDARD: PRT; 866 AA.  
AC Q96f46; 043844;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE Interleukin-17 receptor precursor (IL-17 receptor).  
GN IL17R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell  
RA MEDLINE=98035683; PubMed=9367539;  
RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,  
VandenBos T., Zappone J., Painter S.L., Armitage R.J.;  
RT 'Molecular characterization of the human interleukin (IL)-17  
receptor.';  
RL Cytokine 9:794-800(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
suggesting that additional components are involved in IL17-induced  
signaling.  
CC SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC TISSUE SPECIFICITY: Widely expressed.  
CC PTM: Glycosylated.

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EMBL; U58917; AAB99730.1;

EMBL; BC011624; AAH11624.1;

Genew; HGNC:5985; IL17R.

MIM: 605461;

Receptor; Transmembrane; Signal; Glycoprotein.

FT SIGNAL 1 31 POTENTIAL

FT CHAIN 32 866 INTERLEUKIN-17 RECEPTOR

FT DOMAIN 32 320 EXTRACELLULAR (POTENTIAL)

FT TRANSMEM 321 341 POTENTIAL

FT DOMAIN 342 866 POTENTIAL

FT DOMAIN 810 818 CYTOPLASMIC (POTENTIAL)

FT DOMAIN 49 49 N-LINKED (GLCNAC...)

FT CARBOHYD 49 49 N-LINKED (GLCNAC...)

FT CARBOHYD 54 54 N-LINKED (GLCNAC...)

FT CARBOHYD 206 206 N-LINKED (GLCNAC...)

FT CARBOHYD 225 225 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CONFLICT 367 367 V -> A (IN REF. 1)  
 FT CONFLICT 380 380 H -> R (IN REF. 1)  
 SQ SEQUENCE 866 AA; 96131 MW; 28330BDE2303B0C9 CRC64;

Query Match 13.9%; Score 308; DB 1; Length 866;  
 Best Local Similarity 28.3%; Pred. No. 1.9e-15;  
 Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 EESSESTYTAALPRELRPRP---KVFYSSKQDQNMNVVOCFAFYLDQPCGEVA 69  
 DB 353 EKSDDTKYDGLPVAIDLPPPLPKRWIYSA-DHPLVYDVVLKFAQLLTACGTEVA 411  
 QY 70 LDLEWEDFSLCRGOREWV---TOKIHESQPLIVVCSKMKYFVCKNKYKKGGS-----120  
 DB 412 LDLEWEDFSLCRGOREWV---TOKIHESQPLIVVCSKMKYFVCKNKYKKGGS-----120  
 QY 121 ---RGSGKGLFLVAVSAIAEKLRQAKSSAALSKFIATVP-DYSCBEDVPGILDSTK 176  
 DB 468 RDRGKPVGDLEFTAAMNMLPDFR---PACFTYVVCYFSEVSCDGVDFLGAAPR 522  
 QY 177 YRLMDLPLQCLSHLSRHDGLQPGQHTROG--SRNRYFSKSGSLYVAICNNHOFIDE 234  
 DB 523 YPLMDRFEV---YFRIDPLEMFEGRMHVRLTGDNYLSPGSGRLAALDRFDQVH 580  
 QY 235 EPDWF---KQVFPHPPLRYREPVLKFDGLVNDVCKPQSPDCLAVEA 286  
 DB 581 CPDWFECENLYSNDODAPSLDEEV-FEPLPP-GRGIVKRAPLVRE-PSQACLAIDP 637  
 QY 287 AVLGATGPAQDSOHE-----SQRGGDQDGEARPAALGSA---ALQ 323  
 DB 638 LVGEQGANVAKLEHPLQPCQAPQPLTLVLAEEGALVAAYVEGFLAGAAVRLA 697  
 QY 324 ---PILFTVAGSPDMDPGSGYDSSVPSSELSILPMBSLSTQDTSTSTSVSS 377  
 DB 698 GEGEACPLIGSPAG-----RNSVLF---LPVDEPSPL---GSSTPMASPDLLPEDVR- 745  
 QY 378 SSGLEEPALPALKSLSSGCKADLGC 405  
 DB 746 ---BHLGLMLSLFGSLSCQAOGG 768

## RESULT 2

ID IL17R\_MOUSE STANDARD; PRT: 864 AA.  
 AC Q60943;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Interleukin-17 receptor precursor (IL-17 receptor).  
 GN IL17R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Thymic lymphoma;  
 RX MEDLINE=96111968; PubMed=8777726;  
 RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,  
 RA Coney M.R., Cohen J.I., Spriggs M.K.;  
 RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a  
 novel cytokine receptor."  
 RL Immunity 3:811-821(1995).  
 CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
 CC suggesting that additional components are involved in IL17-induced  
 CC signaling (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
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DR EMBL; G11993; AAC52357.1;  
 MD; MG1107399; IL17R.  
 KW Receptor; Transmembrane; Signal; Glycoprotein.  
 FT SIGNAL 1 31 POTENTIAL.  
 FT CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.  
 FT DOMAIN 32 322 EXTRACELLULAR POTENTIAL.  
 FT TRANSMEM 323 343 POTENTIAL.  
 FT DOMAIN 344 864 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 809 814 POLY-GU.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 206 206 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC) (POTENTIAL).  
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 13.1%; Score 289.5; DB 1; Length 864;  
 Best Local Similarity 25.8%; Pred. No. 4.5e-14;  
 Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 EESSESTYTAALPRELRPRP---KVFYSSKQDQNMNVVOCFAFYLDQPCGEVA 69  
 DB 355-EKGGDSKINGILPVADLPPLRPRKWIYSA-DHPLVYVVLKFAQLLTACGTEVA 413  
 QY 70 LDLEWEDFSLCRGOREWV---TOKIHESQPLIVVCSKMKYFVCKNKYKKGGS-----119  
 DB 414 LDLEWEDFSLCRGOREWV---TOKIHESQPLIVVCSKMKYFVCKNKYKKGGS-----119  
 QY 120 ---GGSGKGLFLVAVSAIAEKLRQAKSSAALSKFIATVPDYSC-BEDVPGILDLS 174  
 DB 469 QLECDENKPVGDLEFTAAMNMLPDFR---PACFTYVVCYFSEVSCDGVDFLGAAPR 523  
 QY 175 YRLMDLPLQCLSHLSRHDGLQPGQHTROG--SRNRYFSKSGSLYVAICNNHOFIDE 232  
 DB 524 YPLMDRFEV---YFRIDPLEMFEGRMHVRLTGDNYLSPGSGRLAALDRFDQVH 581  
 QY 233 DEPDWFEKQVFPHP---PPLR---YRDPLEKFDGLVNDVCKPQSPDCLAVEA 285  
 DB 582 TQCPDWFECENLYSNDODAPSLDEEV-FEPLPP-GRGIVKRAPLVRE-PSQACLAIDP 639  
 QY 286 AVLGATGPAQDSOHE-SQRGGDQDGEARPAALGSAALOPLLH 327  
 DB 640 VCV-----SEESRMALDPLQPCQAPQPLTLVLAEEGALVAAYVEGFLAGAAVRLH 688  
 QY 328 TVVAGSPDMP-RDS-----GITDSSV---PSSELSLPL-----WGLSTDTQT 366  
 DB 689 PDGSGAAQLPMTEDSBACPLGVORNSILCLPVDSDDPLCPSTPMASPDHLDQAREQL 748  
 QY 367 ETSLSLTSVSSSSSGEGEPP-----ALPSKLLSSGCKADLGC 404  
 DB 749 ESLMLSVLQQLSGPLSPVPEVLEGTPESEORQSVSDQG 794

## RESULT 3

ID IL17S\_HUMAN STANDARD; PRT: 502 AA.  
 AC Q9NRU6; Q9NRU6; Q9NRU4; Q9NRU5;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Interleukin-17 receptor precursor (IL-17 receptor) (IL-17 receptor  
 DE homolog 1) (IL-17R1) (IL17R1) (Cytokine receptor CR14).  
 OS Homo sapiens (Human).  
 GN IL17BR OR EV17.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
 OX NCBI TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=10273223; PubMed=10815801;  
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,  
 RA Shaughnessy J.D. Jr.,  
 RT "Evi27 encodes a novel membrane protein with homology to the IL17  
 RL Oncogene 19:2098-2109(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF N-TERMINUS.  
 RX TISSUE=Lung; PubMed=10749887;  
 RC MEDLINE=20317118; PubMed=10749887;  
 RA Shi Y., Ulrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,  
 RA Barber M.C., Wang W., Wathen K., Bodge V., Fisher C.L., Olsen H.,  
 RA Ruben S.M., Knyszev I., Cho Y.H., Kao V., Wilkinson K.A.,  
 RA Carrell J.A., Ebner R.,  
 RT "A novel cytokine receptor-ligand pair. Identification, molecular  
 RL characterization, and in vivo immunomodulatory activity".  
 RN J. Biol. Chem. 275:19167-19176(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Zhang W., Cao X.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Strausberg R.,  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP FUNCTION.  
 RX PubMed=11058597;  
 RA Lee J., Ho W.H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,  
 RA Goddard A.D., Yasuda D.G., Vandlen R.L., Wood W.I., Gurney A.L.,  
 RT "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog  
 RL IL-17Rn1".  
 RN J. Biol. Chem. 276:1660-1664(2001).  
 CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and  
 CC IL17E. May play a role in controlling the growth and/or  
 CC differentiation of hematopoietic cells.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);  
 CC Secreted (isoform 2).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here), and 2; are  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in several endocrine tissues, mostly  
 CC in fetal and adult liver, kidney, pancreas, testis, colon, brain  
 CC and small intestine; not detected in peripheral blood leukocytes,  
 CC lymphoid organs, and most cell lines.  
 CC -----  
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 CC -----  
 CC EMBL; AF208110; AAF86051.1;  
 CC EMBL; AF208111; AAF86052.1;  
 CC EMBL; AF212365; AAF78776.1;  
 CC EMBL; AF250309; AAK37428.1;  
 CC EMBL; BC000980; AAK00980.1;  
 CC Genes; HGNC:18015; IL17ER.  
 DR MIM; 605458;  
 DR Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.  
 KW SIGNAL  
 FT CHAIN 1 17  
 FT DOMAIN 18 502 INTERLEUKIN-17B RECEPTOR.  
 FT TRANSMEM 18 292 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 293 313 POTENTIAL.  
 FT DOMAIN 314 502 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 250 288 --> VEPSELLWGGKGRHRLFHSLRLSSLSNALLPADT  
 FT --> S (IN ISOFORM 2).  
 FT VARSPLIC 289 502 MISSING (IN ISOFORM 2).  
 FT CONFLICT 6 6 L-> I (IN REF. 1).  
 FT CONFLICT 422 426 LPPLA-> SSPCL (IN REF. 2).  
 FT CONFLICT 427 502 MISSING (IN REF. 2).  
 FT CONFLICT 468 468 L-> F (IN REF. 1).  
 SQ SEQUENCE 502 AA: 55984 MW: 5887586FAAE49CC-CRC64;  
 Query Match 5.7%; Score 127.5; DB 1; Length 502;  
 Best Local Similarity 24.6%; Pred. No. 0.03;  
 Matches 45; Conservative 31; Mismatches 92; Indels 15; Gaps 4;  
 QY 8 IYSHLDEESSESTYALPRELRPRPVLCYSSKDGONNNVVOCAFVLODFGCR 67  
 DB 312 MWRERIKTSFTT-----LLPIKLVVPSLGFHH--TICITFELQNHCRSE 362  
 QY 68 VALDMEDFSLCRSGREWIQKHESQIIVVCKGKMYFVKKYKHKGGKSGKGE 127  
 DB 363 VILKRWKKIAKMGPVOMLATOKKAADKVVLLSNVNSVCDGTCGKSGSPSENQ-D 431  
 QY 128 LFLVAVSAIAEKLRQKSSAALSFIATVFDYSCSDVPGILDLSTYRIKMLPOLC 187  
 DB 422 LFLPLNLFCSDLR-----SQIHLHKYVVVVFREIDTKDDYNALSVCPYHLMDATAFC 476  
 QY 188 SHL 190  
 DB 477 AEL 479  
 RESULT 4  
 ID YS02\_CAEEL STANDARD; PRT; 718 AA.  
 AC Q10128;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Hypothetical 81.6 kDa protein F56D1.2 in chromosome II precursor.  
 GN F56D1.2  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Chassee S., Wilson R.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL; U39997; AAA81100.1;  
 DR Wormpep; F56D1.2; C801970.  
 KW Hypothetical protein; Transmembrane; Signal.  
 FT SIGNAL 1 30 POTENTIAL.  
 FT CHAIN 31 718 HYPOTHETICAL PROTEIN F56D1.2.  
 FT TRANSMEM 373 393 POTENTIAL.  
 SQ SEQUENCE 718 AA: 81622 MW: 4289056288417AA CRC64;  
 Query Match 5.7%; Score 126; DB 1; Length 718;  
 Best Local Similarity 21.1%; Pred. No. 0.06;  
 Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;



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DR EMBL; U19521; AA69913.1;  
DR EMBL; D30798; BA19478.1;  
DR MGD; MGI:107362; Stabp3.  
DR InterPro; IPR001619; Sec1-like.  
DR Pfam; PF00995; Sec1.1;  
KW Protein transport.  
SQ SEQUENCE 592 AA; 67942 MW; 7874B71DE10781A CRC64;

Query Match 4.88; Score 105.5; DB 1; Length 592;  
Best Local Similarity 18.88; Pred. No. 1.6; 5;  
Matches 89; Conservative 60; Mismatches 145; Indels 179; Gaps 21;

OY 6 ENYSHLDSESESTYALPRERLRPPKVFICYISKDQHNNVQCFAYLQDFC- 64  
DB 63 ENYFAKREVRQKALIF-----ISPTNSVDFLDFGSKSEKKKAYIIFDFCP 115

OY 65 -----GCE-----VALDLWEDFSLC-----REGQREWIQ 89  
DB 116 DLFENKIKASCSSIRCKEINISFIPQSOVYILDVDAFYCYSPDFSNASKEYVNE 175

OY 90 KIHESQFIIVWC-----SKGMV-----FVDRK---NFK---HKGGRSGSGK 126  
DB 176 AMAEQ--IVVCATLDNPGVRYKSKPLONASKLAQLVKKLEDYKIDKGLKNGTOS 233

OY 177 ELFLV-----AVSAETAKLRQAKSSALSALSFIAVFD-----ISCEG-DVPGI 170  
DB 234 QALLIDRGDPSTVHLEL-----TFQAMAYDLPIENTYKIDKKEAV 281

OY 171 L-----DLSTKYR-----LMDNLPQLCSHLASRDHGLQEPQNTROGSRNFRKSGRS 220  
DB 282 LEEDDLVRYRHRHIAVLEETPKLKEISTK-----KATEGT 332

OY 221 LYVAICNMQFIIDEHPWFQKQVFPFPPPLRYREPVLKEF----- 261  
DB 323 SLGALTQAKKMPHPRKQISKQVY-----HLNLABOCNFKLNIEKLCYEQDALGLTD 377

OY 262 -----DSGLVLDNVMCKPGPDSFCLKVEAAVLGATGPAQSQHSQHGGLDQGEARP 314  
DB 378 AEGQVRKDSMLVLLPVL--KNHNDCKIRAVLLXINGTTEEN----- 422

OY 315 ALDGSAAQPLIHTVKAGSPDMPRD-SGIYDSVPSSELSPLMELGLSTDT 366  
DB 423 -----LDLHNNKIEDSDMRNWSHLGVYVPPSQAKPLKRSARET 468

## RESULT 7

Z151\_MOUSE STANDARD; PRT; 794 AA.  
AC Q60821; Q60699;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Zinc finger protein 151 (Polyomavirus late initiator promoter binding  
DE protein) (LP-1) (Zinc finger protein z13).  
GN ZNF151 OR ZFP100.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
[1]

RN SEQUENCE FROM N.A.  
RA Rapp L., Carmichael G.G.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
[2]

RN SEQUENCE FROM N.A.  
RC STRAIN=CBA; TISSUE=Kidney;  
RX MEDLINE=96003919; PubMed=7575457;  
RA Schultz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;

RT

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\*An unusual arrangement of 13 zinc fingers in the vertebrate gene  
Z13.

Biochem. J. 311:219-224(1995).

-1- FUNCTION: MAY-FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT

REGULATES THE EXPRESSION OF SPECIFIC GENES.

-1- SUBCELLULAR LOCATION: Nuclear (Potential).

-1- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES

EXAMINED.

-1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-

FINGER PROTEINS.

-1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.

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EMBL; U22396; AA64848.1;  
EMBL; U14556; AA85493.1;  
HSP; P08046; IAH.

MGD; MGI:107410; Zfp100.

InterPro; IPR000210; BTB\_POZ.

InterPro; IPR000822; Znf\_C2H2.

Pfam; PF00096; zf-C2H2; 13.

Pfam; PF00651; BTB; 1.

PRINTS; PR00048; ZINCFINGER.

ProDom; PD000003; Znf\_C2H2; 1.

SMART; SM00225; BTB; 1.

SMART; SM00355; Znf\_C2H2; 13.

PROSITE; PS00097; BTB; 1.

PROSITE; PS00026; ZINCFINGER\_C2H2\_1; 13.

PROSITE; PS00157; ZINCFINGER\_C2H2\_2; 13.

Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;

Nuclear protein; Repeat.

DOMAIN 1 104 BTB.

DOMAIN 297 730 ZINC FINGERS.

ZNF\_FING 297 319 C2H2-TYPE.

ZNF\_FING 325 347 C2H2-TYPE.

ZNF\_FING 353 375 C2H2-TYPE.

ZNF\_FING 381 403 C2H2-TYPE.

ZNF\_FING 409 431 C2H2-TYPE.

ZNF\_FING 437 459 C2H2-TYPE.

ZNF\_FING 465 487 C2H2-TYPE.

ZNF\_FING 493 515 C2H2-TYPE.

ZNF\_FING 519 543 C2H2-TYPE.

ZNF\_FING 549 571 C2H2-TYPE.

ZNF\_FING 577 599 C2H2-TYPE.

ZNF\_FING 605 628 C2H2-TYPE.

ZNF\_FING 708 730 C2H2-TYPE.

CONFLICT 507 507 G -> A (IN REF. 2).

CONFLICT 573 573 N -> K (IN REF. 2).

SEQUENCE 794 AA; 86664 MW; PFF8856DEBFTED CRC64;

Query Match 4.54; Score 99.5; DB 1; Length 794;  
Best Local Similarity 20.68; Pred. No. 6.5;  
Matches 71; Conservative 41; Mismatches 146; Indels 87; Gaps 15;

OY 64 CGCEVALDLWEDFSLCREGQREWYIKTHESQFIIVCSKMK-YFVCKENKKGGRG 122

DB 24 CDTFTVVD-GVDF-----KAHKA-VLAACSETFKGLFVQKQDVHLDLSNA 67

OY 123 SGKGLFLVVSATKLRQAKQSSS-----AALSFTIATVFTDSCGDPVGLDLS 175

DB 68 AGLGQ-----VLEFMYTKLSLSPENVDDVLAVASFLQMQ-----DIVT 106

OY 176 KYRLNLPQLCSHL-HSRDRGLQEPQH-----TRQSRNRYFRSKSGSLY 222

DB 107 ACHTLKSLAEPSTTGESADASAVEGDKRDKAAATMLSLGQARGSSSTGFGRELK 166

OY 223 VALCNMQFIIDEHPWFQKQVFPFPPPLRYREPVLKEFQSLGLVLDNVMCKPGPDS 282



Db 167: EERGQAESAGARQTERADAPREPP-----VELKPPDPSSMA- 206  
 QY 283 KYEAVYNGTGPADSHQSHQGLDQGEARPDALGSAALPLLTIVKAGSPDMRPSG 342  
 Db 207 AAEEALSESSEGEVEVPASG--EDGEEGAGPATVKEGSH-LONGEPEENEESA 263  
 QY 343 ITDSSVPSSELSLP---LAEGLSTDTSTSLTESVSSSGIGEE 384  
 Db 264 GTDS---GQELGEGONLRSYTGIDRTESKAYGSIHKCEOGKE 305

## RESULT 8

ABL\_MLVAB STANDARD; PRT; 746 AA. #  
 ID ABL\_MLVAB  
 AC P00521  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transforming protein ABL (EC 2.7.1.112).  
 GN v-abl  
 OS Abelson murine leukemia virus  
 CC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses.  
 CX MCB\_TaxID-11788;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83221648; PubMed-6304726;  
 RA Reddy E.P., Smith M.J., Srinivasan A.;  
 RT "Nucleotide sequence of Abelson murine leukemia virus genome:  
 RT structural similarity of its transforming gene product to other onc  
 RT gene products with tyrosine-specific kinase activity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3623-3627(1983).  
 RN [2]  
 RP REVISIONS TO 588-746.  
 RA Reddy E.P., Smith M.J., Srinivasan A.;  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7372-7372(1983).  
 RN [3]  
 RP SEQUENCE OF 233-327 FROM N.A.  
 RX MEDLINE-83245023; PubMed-6191223;  
 RA Groffen J., Heisterkamp N., Reynolds F.H. Jr., Stephenson J.R.;  
 RT "Homology between phosphotyrosine acceptor site of human c-abl and  
 RT viral oncogene products.";  
 RL Nature 304:167-169(1983).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 CC tyrosine phosphate.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ABL  
 CC POLYPEPTIDE.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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CC EMBL; V01541; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; R00010; AAA46470.1;  
 DR PIR; A00627; TVNVGN.

DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; SH2; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.

DR SMART; SM00219; TyRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00001; SH2; 1.  
 KW Polyprotein; tyrosine-protein kinase; Transferase; Oncogene;  
 SH2 domain.  
 FT DOMAIN 13 103 SH2.  
 FT DOMAIN 128 379 PROTEIN KINASE.  
 FT DOMAIN 128 379 PROTEIN KINASE.  
 SQ SEQUENCE 746 AA; 81872 MW; B9072FF55FE9257 CRC64;

## Query Match 4.4%; Score 96.5; DB 1; Length 746;

Best Local Similarity 20.7%; Pred. No. 10;  
 Matches 90; Conservative 52; Mismatches 165; Indels 147; Gaps 19;  
 QY 49 RMNVVQCF-----YFLDFGCGEVALDLWEDFSLCREGQEWVICKIHESOFIIV 100  
 Db 181 EPNVLQLLGCTREPEPTIITEFTYGNLD-----VLRGNQEVSAVV--LLYMATQ 232  
 QY 101 CSKMKYVDKXNYKKG--GGSGSGKELELYAVSAIA-EKLROAKOSSAALSKE---- 154  
 Db 233 ISSAMET-LEKRNFIHDLAARNCLVGENHLVYADFGLSRLMTGDTTAAHAGAPPIKW 291  
 QY 155 -----IAYFDYSCGDV-----PGILDSTKYRLMNLPLQCLSHLS 192  
 Db 292 TAPESLAYNKFSSIKSDWAPGVLLWEIATYGMSPYGI-DLSQVYELLE----- 339  
 QY 193 RDHGLQBPFGQHTQSGSRNYFR-----SKSGSLXVAICNHHQFIDEE---PDWFER 241  
 Db 340 KDYRMERP-----EGCPKVELARACWNPSPSPAEIHOAFETMFOESSISDEVEK 394  
 QY 242 QP-----VFPHPPLRYREPVLKFDGSLVLDVNMCK-----PGPESDFCLK 283  
 Db 395 ELGKGTGCGAGSMQAPELTKTCTCRAAEQKASPPSLAPKLLRRQVTSPPSSGLSHK 454  
 QY 284 VEMAVLQATC---PADSQ-----HESQGLDQDGEARAL 316  
 Db 455 KENTGASAGMTATAPAPPKNVGLSKASEEMVRRKHSSESPGSD---KGLAK 511  
 QY 317 DGSAAALPLHTVKGSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQTSSTTESVS 376  
 Db 512 LKAPPPPPACTCKAGPAQSQEAGEAGGPTKTKTSLANDAVNTDPTKAGPPGE--- 568  
 QY 377 SSSGIGEEPPALP 390  
 Db 569 ---GLRKPVPSPVP 579

## RESULT 9

HT31\_ARATH STANDARD; PRT; 660 AA.  
 ID HT31\_ARATH  
 AC Q04956;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Homeobox protein HAT3.1.  
 GN HAT3.1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsi  
 CC NCBI\_TaxID-3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94035169; PubMed-8106082;  
 RA Schindler U.; Beckmann H.; Cashmore A.R.;  
 RT "HAT3.1, a novel Arabidopsis homeodomain protein containing a  
 RT conserved cysteine-rich region.";  
 RL Plant J. 4:137-150(1993).  
 CC -1- FUNCTION: BINDS ONLY TO LARGE DNA FRAGMENTS. RECOGNIZES A DNA  
 CC FRAGMENT CARRYING 8 COPIES OF BOX7 MOTIF OF THE LIGHT-INDUCED  
 CC CAB-E PROMOTER OF NICOTIANA PLUMBAGINIFOLIA. ALSO RECOGNIZES  
 CC THE BOX7/M1 MOTIF.

CC 1 SUBCELLULAR LOCATION: Nuclear.  
 CC 2 TISSUE SPECIFICITY: PRIMARILY DETECTED IN ROOT TISSUE.  
 CC 3 SIMILARITY: BELONGS TO THE PHD-ASSOCIATED HOMEBOX FAMILY.  
 CC 4 SIMILARITY: CONTAINS 1 PHD-TYPE ZINC-FINGER.  
 CC 5 SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
 CC 6 This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 CC 13  
 DR EMBL; X69512; CAA49263.1;  
 DR HSSP; P41778; ID06.  
 DR TRANSFAC; T04111;  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR001365; Znf.PHD.  
 DR Pfam; PF00046; homeobox.1.  
 DR Pfam; PF00628; PHD; 1.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR SMART; SM00249; PHD; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 DR PROSITE; PS01359; ZF-PHD.1; 1.  
 DR PROSITE; PS00016; ZF-PHD.2; 1.  
 DR Homeobox; DNA-binding; Nuclear protein; Transcription regulation;  
 KW zinc-finger. 203 259 PHD-TYPE  
 FT ZN\_FING 203 259  
 FT DNA\_BIND 551 610 HOMEBOX.  
 FT SEQUENCE 660 AA; 73604 MW; A3B265CD394DAL38 CRC64;  
 Query Match 4.33; Score 96; DB 1; Length 660;  
 Best Local Similarity 21.48; Pred. No. 9.4; Mismatches 129; Indels 112; Gaps 18;  
 Matches 79; Conservative 49;  
 QY 103 KGMVYFDKNTKH-----GGRGSGKGELEFVAVIAEKLRAQSSAALESFI 155  
 DB 120 KLLRYLFRNTEQSLDAYSLGWGSS-----LEKIPKELERATK----- 164  
 QY 156 AVTFDYSCSDVPGILDLSYKRLNLPGLCSHLHSHRHLGAEQPHQTSRRNFRS 215  
 DB 165 -----ILRSKLLDLFQLDLTLCAGSLPESLFTDGEI-----SSDIFCA 206  
 QY 216 KSG-RSLIV-----MHQIDEEDMFEKGFVFPFPPPLRYRPPVLE-KFDS 263  
 DB 207 KCGSKLSVNDIILCDGFCGRGFCYCLEPP--LRKEDIP--PDDEGLCPGCDCKDS 262  
 QY 264 GLVINDVCKPSPGDFLKV-----EAVLGTATPAD-----SQHES 301  
 DB 263 LLLNLSLTGKESVDSWEKIFPEANALVGGQMLDCLPDSADSDDEYDPCDLNEN 322  
 QY 302 QHGLQDQEARPALDG-----AALQPLHIVKAGS-----PSDMRPDSGIYD 345  
 DB 323 DEQSD-DNEES-ENEDSGSDTEFTSASDEMIESFKGDKIMKVMALPSDSEDDO-YD 380  
 QY 346 SSVPSSELSLPLMEGLTDTDTETSSITESVSSSGIAG-----EPPALPFSKLS 395  
 DB 381 DPATPCD-----DDKSSNSDCTSDTDLTSTFKGDETQQAEDPPLDPCGRTSLOQ 434  
 QY 396 SGCKADLG 404  
 DB 435 DAILESVDG 443  
 RESULT 10  
 PRGR\_HUMAN STANDARD; PRT; 933 AA.  
 AC P06401; Q09PFF;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Progesterone receptor. (PR)  
 GN PGR OR NR33.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 CC NCBI\_Taxid=9606;  
 RN [1]  
 RP MEDLINE; 9028361; PubMed=238727;  
 RA Kastner P., Krust A., Turcotte B., Stropp U., Tori L., Gronemeyer H.,  
 RA Chambon P.;  
 RT "Two distinct estrogen-regulated promoters generate transcripts  
 RT encoding the two functionally different human progesterone receptor  
 RT forms A and B";  
 RL EMBL; J-9:1603-1614(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 87184565; PubMed=3551956;  
 RA Mirzaii M., Atger M., D'Aurilio L., Loosfelt H., Mariel C.,  
 RA Fridlansky F., Guichon-Mantel A., Gallibert E., Milgrom E.;  
 RT "Complete amino acid sequence of the human progesterone receptor  
 RT deduced from cloned cDNA";  
 RL Biochem. Biophys. Res. Commun. 143:740-748(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Kieback D.G., Agoulnik I.U., Tong X.-W.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 682-933;  
 RX MEDLINE; 98282128; PubMed=9620806;  
 RA Williams S.P., Sigler P.B.;  
 RT "Atomic structure of progesterone complexed with its receptor";  
 RL Nature 393:393-396(1998).  
 CC 1-1 FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 CC 1-1 SUBCELLULAR LOCATION: Nuclear.  
 CC 1-1 ALTERNATIVE PRODUCTS: 2 ISOFORMS: A AND B (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC 1-1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC 1-1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 CC NR3 SUBFAMILY.  
 CC 6 This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 CC 7  
 DR EMBL; X51730; CAA36018.1;  
 DR EMBL; M15716; AAA60081.1;  
 DR EMBL; AF016381; AAD01587.1;  
 DR PIR; A03245; QRRUP.  
 DR PIR; S09971; S09971.  
 DR PDB; 1A28; 15-JUL-98.  
 DR TRANSFAC; T00696;  
 DR Genew; HGNC:8910; PGR.  
 DR MIM; 264080;  
 DR InterPro; IPR000536; Hormone\_rec\_lig.  
 DR InterPro; IPR000128; Progesterone\_receptor.  
 DR InterPro; IPR001723; Steroid\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; ZF-C4; 1.  
 DR Pfam; PF02161; Prog\_receptor; 1.  
 DR PRINTS; PR00398; STEROIDOMER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR PRODOM; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOL1; 1.

SMART: SM00399; znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding; Phosphorylation; Alternative splicing;  
 FW 3D-structure; 1 566 MODULATING, PRO-RICH.  
 FT DOMAIN 567 632 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 567 632 C4-TYPE.  
 FT ZN\_FING 603 627 STEROID-BINDING.  
 FT DOMAIN 681 933 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 183 187 PHOSPHORYLATION (BY CK).  
 FT MOD\_RES 227 227 PHOSPHORYLATION (BY CK).  
 FT MOD\_RES 232 232 PHOSPHORYLATION (BY CK).  
 FT MOD\_RES 552 552 PHOSPHORYLATION (BY CK).  
 FT MOD\_RES 793 793 PHOSPHORYLATION (BY CK).  
 FT VARSPLIC 1 164 MISSING (IN ISOFORM A).  
 FT CONFLICT 226 226 G -> S (IN REF. 1).  
 FT CONFLICT 256 256 V -> S (IN REF. 1).  
 FT CONFLICT 344 344 S -> T (IN REF. 1).  
 FT CONFLICT 660 660 L -> V (IN REF. 2).  
 SQ SEQUENCE 933 AA; 98994 MW; 8041487F1F17F8E CRC64;  
 Query Match 4.38; Score 95; DB 1; Length 933;  
 Best Local Similarity 26.04; Pred. No. 17;  
 Matches 46; Conservative 19; Mismatches 66; Indels 46; Gaps 8;  
 QY 270 VMCKP-GP-----ESDFCLKVAAVVGATG-----PADSQHSGHGLDQDQ- 310  
 DB 27 LCRPAAGFPFGSQTSLTPEVSAIPISLDGLLPPRCQGDPSDEKTDQOQSLSDEGA 86  
 QY 311 ----EAPALDGSAAALPILHTVKGSPDMRDSGIYDSSVPSSELSLPLMGLSLTDQ 366  
 DB 87 YSRAETRGAGGSSSP-----EKDGLDLSVLDLTLAAGSGQSQSP 131  
 QY 367 ETSSLTSSVSSSGLGREPPALP-----SKLLSGCKFNDLGRSTYDELHAP 417  
 DB 132 PACVTSWCLFGPELPEDPPAPATQVLSPLMSRGCK--VGDSSGTAARHVL 186  
 RESULT 11  
 ID 1863 MCMVS STANDARD; PRT; 841 AA.  
 AC Q69154;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Transcriptional regulator 1863 homolog (Protein UL69).  
 GN UL69.  
 OS Murine cytomegalovirus (strain Smith).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Murine cytomegalovirus.  
 OX NCBI\_TaxID=10367;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96082764; PubMed=7483291;  
 RA Messierle M., Kapp M., Lucin P., Koszinski U.B.;  
 RT "Characterization of a conserved gene block in the murine  
 cytomegalovirus genome."  
 RL Virus Genes 10:73-80(1995).  
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,  
 HSV-2 UL54, HSV-1 5, VZV 4, EBV BMFL1, HVS-1 57, HCMV AND MCMV  
 UL69.  
 CC  
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 CC EMBL; L07319; AAA96666.1;

KW Transcription regulation.  
 SQ SEQUENCE 841 AA; 92706 MW; 9F18372739D723E4 CRC64;  
 Query Match 4.38; Score 94.5; DB 1; Length 841;  
 Best Local Similarity 23.14; Pred. No. 16;  
 Matches 58; Conservative 25; Mismatches 73; Indels 95; Gaps 13;  
 QY 192 SDHGLAQEQHTQGR--NFRSGSGSLYVAICNH----- 229  
 DB 536 SRRSSATDGRSGRSGRGAQSRNGHSSSPST--VSTTVHGQNGAGDSAPSRK 593  
 QY 230 -QFDEPDMFERQ---FVPPFPPLRYREPVLEKFDGLVNDVMCKPQSPDFCLAVE 285  
 DB 594 SQSQSQQPTTSKSSKTAAMPSP-----SP-----CSPSPAS----- 627  
 QY 286 AAVLGATPADSQHSGHGLDQDGEARPALDGSAAALPILHTVKGSPDMPRD---SG 342  
 DB 628 -----RERRPSKSPSSSPR--HDPPSGEPADAEKELATAG 661  
 QY 343 IYDSSVPS-SELSLPLMGLSLTDQETSSLTSSVSSSGSGEERPPA-----LPSKLL 394  
 DB 662 DEDEGVSPGECVATRGSSADESSSSSSSSSSSSS-DEESDYEDCRLDLSKRL 720  
 QY 395 SSG---SCKAD 402  
 DB 721 EEALERCERD 731  
 RESULT 12  
 ID RMIL\_CHICK STANDARD; PRT; 806 AA.  
 AC Q04982;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE RMIL serine/threonine-protein kinase (EC 2.7.1.37).  
 GN C-RMIL.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphocytes, and Fibroblast;  
 RX MEDLINE=93312327; PubMed=8323553;  
 RA Calogeraki I., Barner J.V., Eychene A., Felder M., Catthy G.,  
 Marx M.;  
 RT "Genomic organization and nucleotide sequence of the coding region of  
 the chicken c-Rm11(B-raf-1) proto-oncogene."  
 RL Biochem. Biophys. Res. Commun. 193:1324-1331(1993).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN  
 NEURAL CELLS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
 SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.  
 CC -1- PTM: PHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: BELONGS TO THE MIL/RAF SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
 BINDING DOMAIN.  
 CC  
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 CC EMBL; X67052; CAA47436.1;





OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=9726110; PubMed=9107688;  
 RA Taylor C., Wadey R., O'Donnell H., Roberts C., Mattei M.-G.,  
 RA Kimber W.L., Wynshaw-Boris A., Scambler P.J.;  
 RT "Cloning and mapping of murine Dgcr2 and its homology to the Sez-12  
 RL seizure-related protein.";  
 RM Mamm. Genome 8:371-375(1997).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain cortex;  
 RX MEDLINE=9621297; PubMed=8630060;  
 RA Kajiwara K., Nagasawa H., Shimizu-Nishikawa S., Ookura T.,  
 RA Kimura M., Sugaya E.;  
 RT "Cloning of Sez-12 encoding seizure-related and membrane-bound  
 RL adhesion protein.";  
 CC -!- FUNCTION: PROBABLY PLAYS A ROLE IN NEURAL CREST CELL MIGRATION.  
 CC MAY PLAY A ROLE IN DELIVERY OF EXTRACELLULAR SIGNALS.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Ubiquitous in various organs with low  
 CC ABUNDANCE.  
 CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 VNFC DOMAIN.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
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 DR EMBL; X95480; CAA64749.1; ;  
 DR EMBL; D78641; BAAL1460.1; ;  
 DR HSP; P01130; IAJJ.  
 DR MGI; MGI:892866; Dgsc.  
 DR InterPro; IPR002172; LDL\_recept\_A.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR001007; VNF\_C.  
 DR Pfam; PF00057; ldl\_recept\_a; 1.  
 DR Pfam; PF00059; lectin\_c; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR SMART; SM00192; LDLA; 1.  
 DR SMART; SM00214; VNC; 1.  
 DR PROSITE; PS01208; VNF\_C; 1.  
 DR PROSITE; PS01209; LDLA\_1; 1.  
 DR PROSITE; PS00068; LDLA\_2; 1.  
 DR PROSITE; PS00041; C\_TYFE\_LLECTIN\_2; 1.  
 DR Receptor; Glycoprotein; Transmembrane; Lectin; Signal.  
 FT SIGNAL  
 FT CHAIN 1 24 POTENTIAL.  
 FT DOMAIN 25 548 INTEGRAL MEMBRANE PROTEIN DGC2/IDD.  
 FT DOMAIN 348 366 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 348 366 POTENTIAL.  
 FT DOMAIN 367 548 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 28 68 LDL-RECEPTOR CLASS A.  
 FT DOMAIN 113 239 C-TYPE LECTIN.  
 FT DOMAIN 268 331 VNF\_C.  
 FT DISULFID 30 44 BY SIMILARITY.  
 FT DISULFID 37 57 BY SIMILARITY.  
 FT DISULFID 51 66 BY SIMILARITY.  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 194 194 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 167 67 P -> PE (IN REF. 2).  
 FT CONFLICT 108 111 SEIG -> R (IN REF. 2).  
 FT CONFLICT 370 370 A -> R (IN REF. 2).  
 SQ SEQUENCE 548 AA; 50697 MW; 77AF5CA839F6B817 CRC64;  
 Query Match 4.2%; Score 92.5; DB 1; Length 548;  
 Best Local Similarity 19.5%; Pred. No. 14;

Matches 87; Conservative 48; Mismatches 114; Indels 197; Gaps 24;  
 QY 73 WEDFSICREGQRE-WVTKIHESQFIIVVCSGKMYFVDKNTKKGGRSGRGK--ELF 129  
 DB 176 WKD-----QRKLWV-----GYQVITGRNLSLEGREWEVAFKGSPEVF 212  
 QY 130 L-----VAVSAIAEK-----LRQAKOSSAALSFIAY-----158  
 DB 213 LPDPIFASANSENDNVFCAQLQCFHPTLRHDLRSHWAESCSEKSFACKRSQTCVDI 272  
 QY 159 -----FDYSCGDVFGILDLSYRLMDNLPLCL-SHLHSDRDLQEPQCHTRO--- 206  
 DB 273 KDNVDEGFYTFPKGDDPCL--SCTCHR--GEPEMCVVALCERPGCQYKPKCK 337  
 QY 207 -----GSRNRYFSKSGSLYVAIC-----NM 228  
 DB 328 FMCIDPDGS--SLFDSRSGMRIVVSCISSFLILSLFVHRLAQRRIEISLIGANL 385  
 QY 229 HQF-----IDEEPWFKEQFVPPH-----PPPLYRFPVLEKFDG 264  
 DB 386 BHFNLGRRIPGDTGPDGFGTGLTPLHLSDDGEGTFHFHDPPPTTAYKYDMDQDD- 444  
 QY 265 LVLYDMYCKPGPESDFCLRYEAAVLGATGPDADSQHSGHGLDQGEARPALDGSAAALQ 324  
 DB 445 -----PPPYEASINPDSVFT---DPADDD-----AFEP 470  
 QY 325 LLHTVKAGSPSDMPDSCI-----YDSVPSSELSPLMEGLSTOOTETSSL-----TE 373  
 DB 471 -----VEASLPA--PRDGGIEGALPRELDQPLPPAFTSLADLE---DSTDSSALLVPPD 520  
 QY 374 SVSSSSGLGESEPPA---LPSKLLSS 396  
 DB 521 PAOSGSTPATEAPPGGRLPRASLNT 546

Search completed: May 19, 2003, 09:21:01  
 Job time : 14.4873 secs





GenCore version 5.1.4.p5.4578  
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OM protein : protein search, using .sw model

Run on: May 19, 2003, 09:17:08 ; Search time 11.3807 seconds  
(without alignments)  
1080.669 Million cell updates/sec

Title: US-09-912-157-2\_COPY\_336\_753

Perfect score: 2210  
Sequence: 1 RKKQENIYSHLDESSSS.....CRADLGCSYDELAVAL 418

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:  
5: /cgn2\_6/ptodata/1/1aa/PCFUS\_COMB.pep:  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	14.0	866	2	US-08-620-694A-10
2	310	14.0	866	3	US-09-022-255-10
3	310	14.0	866	3	US-09-022-696-10
4	310	14.0	866	3	US-08-978-773-4
5	310	14.0	866	3	US-09-022-253-10
6	310	14.0	866	3	US-09-022-260-10
7	310	14.0	866	4	US-09-022-259-10
8	310	14.0	866	4	US-09-022-257-10
9	289.5	13.1	864	2	US-08-620-694A-2
10	289.5	13.1	864	3	US-09-022-255-2
11	289.5	13.1	864	3	US-09-022-696-2
12	289.5	13.1	864	3	US-08-978-773-2
13	289.5	13.1	864	3	US-09-022-253-2
14	289.5	13.1	864	3	US-09-022-260-2
15	289.5	13.1	864	3	US-09-022-259-2
16	289.5	13.1	864	4	US-09-022-257-2
17	95	4.3	933	4	US-08-764-870-14
18	95	4.3	933	4	US-08-980-113-14
19	92.5	4.2	347	4	US-08-630-915A-32
20	92.5	4.2	2308	1	US-08-015-973-1
21	92.5	4.2	2308	2	US-08-448-164-1
22	92.5	4.2	2308	4	US-08-081-929-2
23	92.5	4.2	2314	4	US-09-816-703A-2
24	91.5	4.1	828	2	US-08-993-228-21
25	90	4.1	803	4	US-09-063-035-2
26	88.5	4.0	830	4	US-09-562-737-31
27	88.5	4.0	2353	4	US-08-984-709A-50

28	88	4.0	410	4	US-08-725-758A-4	Sequence 4, Appl1
29	88	4.0	426	4	US-08-725-758A-2	Sequence 2, Appl1
30	87.5	4.0	683	4	US-09-620-412C-357	Sequence 357, App
31	87.5	4.0	830	4	US-09-562-737-34	Sequence 34, Appl1
32	87	3.9	830	4	US-08-162-809-2	Sequence 2, Appl1
33	87	3.9	951	1	US-09-188-930-303	Sequence 303, App
34	86.5	3.9	617	4	US-09-110-517-2	Sequence 2, Appl1
35	86.5	3.9	1581	4	US-08-466-390-4	Sequence 4, Appl1
36	86.5	3.9	2101	1	US-08-467-781-4	Sequence 4, Appl1
37	86.5	3.9	2101	1	US-08-467-781-4	Sequence 4, Appl1
38	86.5	3.9	2101	1	US-08-467-781-4	Sequence 4, Appl1
39	86.5	3.9	2101	1	US-08-467-781-4	Sequence 4, Appl1
40	86.5	3.9	2101	2	US-08-467-781-4	Sequence 4, Appl1
41	86.5	3.9	2101	4	US-09-452-294-1	Sequence 1, Appl1
42	86.5	3.9	2101	5	PCT-US93-06160-4	Sequence 4, Appl1
43	86	3.9	878	4	US-09-141-212-8	Sequence 8, Appl1
44	86	3.9	878	4	US-09-561-138-8	Sequence 8, Appl1
45	86	3.9	879	4	US-09-141-212-6	Sequence 6, Appl1

## ALIGNMENTS

RESULT 1  
US-08-620-694A-10  
; Sequence 10, Application US/08620694A  
; Patent No. 5869286  
; GENERAL INFORMATION:  
; APPLICANT: Yao, Zhengbin  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Fanelow, William  
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple Power Macintosh  
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; FILING DATE: 21 MARCH 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/538,765  
; FILING DATE: 7 AUGUST 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/410,535  
; FILING DATE: 23 MARCH 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,695  
; REFERENCE/DOCKET NUMBER: 2617-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-620-694A-10

Query Match

14.0% Score 310; DB 2; Length 866;

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Best Local Similarity 28.3%; Pred. No. 8.9e-24;
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 ESSSESTYTAALPRELEPRP---KVFCTSSKQGNHNVVOCFAFLDFQCGCEVA 69
Db 353 EKSDDTKYTDGLPAADLPPPLPKRYWIIISA-DHPLYVDVVLFAQELLTACGTVA 411
QY 70 LDLMEDFSLCRBQREWV---IQIHESQFIIVVCSKGMKYFDVKKTKHKGCG 120
Db 412 LDLEEQALISEAGVMTVVGROKQKQKVESNKIIVLCRGRTR---AKWQALLGRGAPVRL 467
QY 121 ---RSGSGELFLVAVSAIAEKLQAKQSSAALSFKFIATVF-DYSCGDVPGILDLSK 176
Db 468 RCDHGKPVGDLFTAAANMLPDKF---PACFGTYVVCYFSEVSCDGVDPDLFCAAPR 522
QY 177 YRLMDNLPLQCSHLHSRDLGCEPQHTROG--SRNTYFRSKSGSLYVAICNMHQFIDE 234
Db 523 YPLMDREFEV-YFRIQDLEMPQGRMHRVGLSGDNTLSPGQRLAALDRFRDMQVR 580
QY 235 EPMDFE-----KQFVFPHPPLRYEPVLEKFDGSLVLDVNCYKPGPESDFCLKVEA 286
Db 581 CPMDFECENLISADDDAPSLDEEV-FEELPLPP-GTGVKRAPLVRE-PSQACLAIDP 637
QY 287 AVLGATGPADSOHE-----SQGGIDQDGEARPALDGS---ALQ 323
Db 638 LVGEBGAAVAKLEPHLPQGPAPQPLHTLVLAABEGALVAVEPGPLADGAARLALA 697
QY 324 -----PLIHTVAGSPDMRDSGYDSSVSPSELSPLPMEGLSTDTQETSSLESVSS 377
Db 698 GEGEACPLGSPGAG-----RNSVLF--LPVDPEDSPL--GSSTPMASPOLLPEDVR- 745
QY 378 SSGICEEPPLPALSKLLSGSCADLGC 405
Db 746 -----EHLEGLMLSLFESQSLSCQAQGGC 768

RESULT 2
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Rao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695

```

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REFERENCE/DOCIDET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-10

Query Match 14.0%; Score 310; DB 3; Length 866;
Best Local Similarity 28.3%; Pred. No. 8.9e-24;
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 ESSSESTYTAALPRELEPRP---KVFCTSSKQGNHNVVOCFAFLDFQCGCEVA 69
Db 353 EKSDDTKYTDGLPAADLPPPLPKRYWIIISA-DHPLYVDVVLFAQELLTACGTVA 411
QY 70 LDLMEDFSLCRBQREWV---IQIHESQFIIVVCSKGMKYFDVKKTKHKGCG 120
Db 412 LDLEEQALISEAGVMTVVGROKQKQKVESNKIIVLCRGRTR---AKWQALLGRGAPVRL 467
QY 121 ---RSGSGELFLVAVSAIAEKLQAKQSSAALSFKFIATVF-DYSCGDVPGILDLSK 176
Db 468 RCDHGKPVGDLFTAAANMLPDKF---PACFGTYVVCYFSEVSCDGVDPDLFCAAPR 522
QY 177 YRLMDNLPLQCSHLHSRDLGCEPQHTROG--SRNTYFRSKSGSLYVAICNMHQFIDE 234
Db 523 YPLMDREFEV-YFRIQDLEMPQGRMHRVGLSGDNTLSPGQRLAALDRFRDMQVR 580
QY 235 EPMDFE-----KQFVFPHPPLRYEPVLEKFDGSLVLDVNCYKPGPESDFCLKVEA 286
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QY 324 -----PLIHTVAGSPDMRDSGYDSSVSPSELSPLPMEGLSTDTQETSSLESVSS 377
Db 698 GEGEACPLGSPGAG-----RNSVLF--LPVDPEDSPL--GSSTPMASPOLLPEDVR- 745
QY 378 SSGICEEPPLPALSKLLSGSCADLGC 405
Db 746 -----EHLEGLMLSLFESQSLSCQAQGGC 768

RESULT 3
US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Rao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION NUMBER: US/09/022,696

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FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-696-10

Query Match 14.08; Score 310; DB 3; Length 866;  
Best Local Similarity 28.38; Pred. No. 8.9e-24;  
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 EESSESTTAAALPRERLRPRP----KVFICYSSKQGNHNVVOCFAVFLQDFCGGEVA 69  
DB 353 EKYSDDTKYTGDLPAADLIPPLPKRWIIYSA-DHPLVYDVVLKFAQLLTACGTEVA 411  
QY 70 LDWEDFSLCRGQREW----IQKHESQFIIVVCSKGMKYFVDKKNYKHGG-----120  
DB 412 LDLEEQATSEAGVNTVGRQKQWESKSIIVLCSSGTR----AKQALLGRGAPVRL 457  
QY 121 ----RSGSGELFLVAVSAIAERKRAKQSSAALSKEFIATVF-DYSCBQDVPGLDLSK 176  
DB 468 RCDHGPVGLDFTAMNMILPDKR----PACFGTVVVCYFSEVSCDGDVDFLGAAPR 522  
QY 177 YRLMDNLPCLSHLSRDHGLQEPGQTRQG--SRNRYFRSKSGSLVIAICNMHQFIDE 234  
DB 523 YPLMDREFV--YFRIQDLEKFGPGHVRVSGELSGDNLSPGPGROLRAALDRFDQVR 580  
QY 235 EPWFE-----KQVFPHPPLPPIREPVLEKFDGLVNDVCKPGPESDFCLKVEA 286  
DB 581 CPWFECENLYSADDOAPSLDEEV-FEPLLP--GTGIKRAPLVRE-PGSOACLAIDP 637  
QY 287 AVLGATGPADSQHE-----SQHGGLDQDGEARPAIDGSA---ALQ 323  
DB 638 LVGEGGAVALKLEPHLQPCQPAPQLHTLVLAEEGALVAVEPGPLADGAARLALA 697  
QY 324 -----PLLTAKGPSMDPRSGIYDSSVPSSLSLPLMEGLSTQDTSTSSITSEVSS 377  
DB 698 GEGEACPLGSPGAG-----RNSVLF---LPVDPEDSPL--GSSTPMASPDLLPEDVR -745  
QY 378 SSGGEEPPALPSKLLSSGSKADLGC 405  
DB 746 -----EHLGLMLSLFQSLSCQAQGC 768

## RESULT 4

US-08-978-773-4  
Sequence 4, Application US/08978773  
Patent No. 6083906  
GENERAL INFORMATION:  
APPLICANT: Troutt, Anthony  
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street

CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER-READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple PowerMacintosh  
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,773  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/052,525  
FILING DATE: 27 NOVEMBER 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2623-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-773-4

Query Match 14.08; Score 310; DB 3; Length 866;  
Best Local Similarity 28.38; Pred. No. 8.9e-24;  
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 EESSESTTAAALPRERLRPRP----KVFICYSSKQGNHNVVOCFAVFLQDFCGGEVA 69  
DB 353 EKYSDDTKYTGDLPAADLIPPLPKRWIIYSA-DHPLVYDVVLKFAQLLTACGTEVA 411  
QY 70 LDWEDFSLCRGQREW----IQKHESQFIIVVCSKGMKYFVDKKNYKHGG-----120  
DB 412 LDLEEQATSEAGVNTVGRQKQWESKSIIVLCSSGTR----AKQALLGRGAPVRL 467  
QY 121 ----RSGSGELFLVAVSAIAERKRAKQSSAALSKEFIATVF-DYSCBQDVPGLDLSK 176  
DB 468 RCDHGPVGLDFTAMNMILPDKR----PACFGTVVVCYFSEVSCDGDVDFLGAAPR 522  
QY 177 YRLMDNLPCLSHLSRDHGLQEPGQTRQG--SRNRYFRSKSGSLVIAICNMHQFIDE 234  
DB 523 YPLMDREFV--YFRIQDLEKFGPGHVRVSGELSGDNLSPGPGROLRAALDRFDQVR 580  
QY 235 EPWFE-----KQVFPHPPLPPIREPVLEKFDGLVNDVCKPGPESDFCLKVEA 286  
DB 581 CPWFECENLYSADDOAPSLDEEV-FEPLLP--GTGIKRAPLVRE-PGSOACLAIDP 637  
QY 287 AVLGATGPADSQHE-----SQHGGLDQDGEARPAIDGSA---ALQ 323  
DB 638 LVGEGGAVALKLEPHLQPCQPAPQLHTLVLAEEGALVAVEPGPLADGAARLALA 697  
QY 324 -----PLLTAKGPSMDPRSGIYDSSVPSSLSLPLMEGLSTQDTSTSSITSEVSS 377  
DB 698 GEGEACPLGSPGAG-----RNSVLF---LPVDPEDSPL--GSSTPMASPDLLPEDVR -745  
QY 378 SSGGEEPPALPSKLLSSGSKADLGC 405  
DB 746 -----EHLGLMLSLFQSLSCQAQGC 768

## RESULT 5

US-09-022-253-10  
Sequence 10, Application US/09022253  
Patent No. 6096305

GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Faselow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-253-10

Query Match 14.0%; Score 310; DB 3; Length 866;  
Best Local Similarity 28.3%; Pred. No. 8.9e-24;  
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 ESSESSTYTAALPRERLRPR-----KVFCLYSKDGQNNHNVOCFAVFLQDFGCEVA 69  
DB 353 EYSDTYTIDGLPADLPPLKPKWIIYSA-DHPLYVDVVLKFAQLLFACTGEVA 411  
QY 70 LQWEDFSLCREGQREWV-----IQKHESOFIIVVCSKGMKYFDVKKNYKHGGG-----120  
DB 412 LLLLEQAISAGVMTWVGROKQENVSNIIVLCSGTR-----AKWQALLGRGAPVRL 467  
QY 121 ---RGSRGKGLFLVAVSAIAEKLRQAKQSSAALSFKIAVYF-DYSCGQVPGILDSTK 176  
DB 468 RCHGKPKVGDLETAANNMILPFK-----PACFGTYVYCYFEVSCDGVDPDLGAAPR 522  
QY 177 IRLNLPOLCSLHSDHGLQEGHTRQ--SRNRYFRSKSGSLVLAICNKHOFIDE 234  
DB 523 YPLADRFEEV-YRIODLEMPQGMHVEGELSGNYLSRSGRLAALDRFQWVR 580  
QY 235 EPQNTS-----KQVFPHPPLRTPREVLKFDGSLVLDVNMCKPFGSPDFCLKVEA 286  
DB 581 CPWFECENLVSADQDQAFSLDEEV-FEELPLP-GTGIVKRAPLVE-FGSQACLAIDP 637  
QY 287 AVLGATGPADSGHE-----SQHGGLDQDGEARFALDGSA---ALQ 323

DB 638 LVGEGGAAXKLEPHLPQGPAPQPLETLVLAABEGALVAAVPGPLADGAARLALA 697  
QY 324 -----PLLTVKAGSPDMPSGIYDSSVSPSSLSLPLMEGLSTQDETETSSLTESVSS 377  
DB 698 GEGEACPLGSPGAG-----RNSVLE---LPVDEDSPL--GSSTPMASPDLLPEDVR- 745  
QY 378 SSGIGREPPALPSKLLSSGSKRADLGC 405  
DB 746 -----EHLGELMLSLFEQSLSCQKQGGC 768

## RESULT 6

US-09-022-260-10  
Sequence 10, Application US/09022260  
Patent No. 6100235

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Faselow, William  
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-260-10

Query Match 14.0%; Score 310; DB 3; Length 866;

Best Local Similarity 28.3%; Pred. No. 8.9e-24;

Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;

QY 14 ESSESSTYTAALPRERLRPR-----KVFCLYSKDGQNNHNVOCFAVFLQDFGCEVA 69  
DB 353 EYSDTYTIDGLPADLPPLKPKWIIYSA-DHPLYVDVVLKFAQLLFACTGEVA 411  
QY 70 LQWEDFSLCREGQREWV-----IQKHESOFIIVVCSKGMKYFDVKKNYKHGGG-----120  
DB 412 LLLLEQAISAGVMTWVGROKQENVSNIIVLCSGTR-----AKWQALLGRGAPVRL 467  
QY 121 ---RGSRGKGLFLVAVSAIAEKLRQAKQSSAALSFKIAVYF-DYSCGQVPGILDSTK 176

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Db 468 RCHGKPVGDLFTANNMLLPDKR-----PACFGTVVCFSEVSCDGDVDFLGAAPR 522
QY 177 YRLMNLPLCZSHLSRDLGLOPQHTROG--SRNRYFSKSGSLVAICNNHOFIDE 234
Db 523 YPLMDRFEV--YFRIOLEMFOPGMRHVGELSGDNTLSPGQRLBAALDRFQOVR 580
QY 235 EPDWER-----KQVFPFHPPLRYEPVLEKFDGSLVNDVCKPSPESDFCLKVEA 286
Db 581 CPDWFECENLYSADDQDAPSLDEEV--FPEPLPP--GTGIVKRAPIVRE--PGSOACLAIDP 637
QY 287 AVLGATGPADSOHE-----SOHGGLDQDGEARPAIDGSA---ALQ 323
Db 638 LVGEBGGAANKLEPHLPQPGOPAPQPLTLVLAEEGALVAAPVPGPLADGAARLALA 697
QY 324 -----PLHTVKGASPDMPDSGIDTSVPSSELSPLMEGLSTOOTETSSLTSSVS 377
Db 698 GECEACPLLGSGAG-----RNSVLF--LPVDPEDSP--GSSTPMASPDLLPEDVR 745
QY 378 SSGLEEEPPALPSKLLSSGCKADIGC 405
Db 746 -----EHLEGLMLSLFEQSLSCOAQGC 768

RESULT 7
US-09-022-259-10
; Sequence 10, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-259-10

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Query Match: 14.0%; Score 310; DB 4; Length 866;
Best Local Similarity 28.3%; Pred. No. 8.9e-24;
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;
QY 14 ESSSSSTTTAALPRRLPRP-----KYFLCYSKDQGHMNVVOCFAYFLQDFCCVEA 69
Db 353 EKYSDTNTYTDGLPAADLPPPLKPKRWIISA--DEPLVDVVLKFAQLTACGTVEA 411
QY 70 LQLEWDFSLCHREGQREWV---IQIHESOFIVVCSKGMKYFVDKKNYKHGGG----- 120
Db 412 LQLEEQALSEAGVNTWGRKQENVESNSKIIVLCRGTR---AKWQALLGRGAPVRL 467
QY 121-----RSGGELFLVAVSAEKLROAKOSSAALSFIATVF--DYSCGDVPGILDLSYK 176
Db 468 RCHGKPVGDLFTANNMLLPDKR-----PACFGTVVCFSEVSCDGDVDFLGAAPR 522
QY 177 YRLMNLPLCZSHLSRDLGLOPQHTROG--SRNRYFSKSGSLVAICNNHOFIDE 234
Db 523 YPLMDRFEV--YFRIOLEMFOPGMRHVGELSGDNTLSPGQRLBAALDRFQOVR 580
QY 235 EPDWER-----KQVFPFHPPLRYEPVLEKFDGSLVNDVCKPSPESDFCLKVEA 286
Db 581 CPDWFECENLYSADDQDAPSLDEEV--FPEPLPP--GTGIVKRAPIVRE--PGSOACLAIDP 637
QY 287 AVLGATGPADSOHE-----SOHGGLDQDGEARPAIDGSA---ALQ 323
Db 638 LVGEBGGAANKLEPHLPQPGOPAPQPLTLVLAEEGALVAAPVPGPLADGAARLALA 697
QY 324 -----PLHTVKGASPDMPDSGIDTSVPSSELSPLMEGLSTOOTETSSLTSSVS 377
Db 698 GECEACPLLGSGAG-----RNSVLF--LPVDPEDSP--GSSTPMASPDLLPEDVR 745
QY 378 SSGLEEEPPALPSKLLSSGCKADIGC 405
Db 746 -----EHLEGLMLSLFEQSLSCOAQGC 768

RESULT 8
US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne

```

REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-257-10

Query Match 14.0%; Score 310; DB 4; Length 866;  
Best Local Similarity 28.3%; Pred. No. 8.9e-243  
Matches 127; Conservative 60; Mismatches 173; Indels 88; Gaps 20;  
QY 14 EESSESTYTAALPRELRPRP---KVFICYSSKQGMHNVVOCFAIFLQDFGCEVA 69  
DB 353 EKYSDTKYTDGLPAADLIPPLPKRKVIYISA-DHPLAVDVVLKFAQLLTAGTEVA 411  
QY 70 LQLEWDFSLCRGQREKV---IQIHESQRLIVVCSKGMKYFVDKKNYKHGG--- 120  
DB 412 LQLEWDFSLCRGQREKV---IQIHESQRLIVVCSKGMKYFVDKKNYKHGG--- 120  
QY 121 ---RSGSGELFLVAVSAIAEKLQKAKOSSAALSKEFIATVYF-DYSCGDVPGTLDLSTK 176  
DB 468 RCDGEPKVDGLFTAMNNILPDKR-----PACFGTVVVCYFSEVSCDGDVDFLGAAPR 522  
QY 177 YRLMDLMLPOLCSHLSHRDGLQEPQ---SRNTYFSKSGSLVAICNNHQFI 232  
DB 523 YPLMDRFEV---YFIQDLENFQGRHVRVGLSGDNTLSPGRLRAALDRFQVNR 580  
QY 235 EPDWE---KQVFPHPPLRYREPVLKFDGLVNDVCMKPGPESDPLKAVEA 286  
DB 591 CPDWECEENLQADQAPSLDEEV-FEPLLP-GTGVKRAPLVRE-PCSQACLAIDP 637  
QY 287 AVLGATGAPDSOHE-----SREGGLQDQGEARALDSSA---ALQ 323  
DB 638 LVGEEGAVALLEPHLQPGQAPAPOLHTLVLAEEGALVAAREVGLADGAVRLALA 697  
QY 324 -----PLLHTVAGSPEDMPDGYSDVSSVPSSELSPLAGLESTDTOTSSITSEVSS 377  
DB 698 GEGEACPLGSGAG-----RNSVLF---LPVDPEDSPL--GSSPTMASPDLLPEDVR- 745  
QY 378 SSGIGSEEPPLPSKLLSSGSKADLGC 405  
DB 746 -----EHLGLMLSLFQSLSCQAQGGC 768

RESULT 9  
US-08-620-694A-2  
Sequence 2, Application US/08620694A  
Patent No. 5869286  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Petkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-620-694A-2

Query Match 13.1%; Score 289.5; DB 2; Length 864;  
Best Local Similarity 25.8%; Pred. No. 1.4e-21;  
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;  
QY 14 EESSESTYTAALPRELRPRP---KVFICYSSKQGMHNVVOCFAIFLQDFGCEVA 69  
DB 355 EKGGDSKINGILFVADLTPPLPRKVIYISA-DHPLVVEVLKFAQLLTAGTEVA 413  
QY 70 LQLEWDFSLCRGQREKV---IQIHESQRLIVVCSKGMKYFVDKKNYKHGG--- 119  
DB 414 LQLEWDFSLCRGQREKV---IQIHESQRLIVVCSKGMKYFVDKKNYKHGG--- 119  
QY 120 ---RSGSGELFLVAVSAIAEKLQKAKOSSAALSKEFIATVYF-DYSCGDVPGTLDL 174  
DB 469 QLECDHWKPADLFTAMNNILPDKR-----PACFGTVVVCYFSEVSCDGDVDFL 523  
QY 175 ---KRYLMDLMLPOLCSHLSHRDGLQEPQ---HTROGSRNTYFSKSGSLVAICNNHQFI 232  
DB 524 SRYPLMDRFEV---YFIQDLENFQGRHVRVGLSGDNTLSPGRLRAALDRFQVNR 581  
QY 233 DEEPDWEKQVFPHP---PPLR---YREPVLKFDGLVNDVCMKPGPESDPLKAVEA 285  
DB 582 TQCPDWEFERMLCLADGDLPLSDEEVDFEPLPP-GGGIVKQAPLVRELP-SDGCLWYD 639  
QY 286 AAVLGATGAPDSOHEOGLQD-----GEARALDSSAALSKEFIATVYF-DYSCGDVPGTLDL 327  
DB 640 VCV-----SEESRMAKLDPOLPQRELVAHTLQSMVLPKQVPA---AVVPEPLHL 688  
QY 328 TVKAGSPDMP-RDS-----GIYDSSV---PSSELSPL-----NGLSTDTOT 366  
DB 689 PDGSGAAQLPWTSEACPLGVQVNSILCLPVSDDPLCLSTPMASPDHLODAREQL 748  
QY 367 ETSSTVTSVSSSGIGSEEP---ALPSKLLSSGSKADLGC 404  
DB 749 ESLMLSVLQQLSLSCQPLESWPFEVVLGCTPSEEBEQRVSQSDQG 794  
RESULT 10  
US-09-022-255-2  
Sequence 2, Application US/09022255  
Patent No. 6072033  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,255

FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/620,694  
FILING DATE: 21 MARCH 1996  
APPLICATION NUMBER: USN 08/538,765  
FILING DATE: 7 AUGUST 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-09-022-253-2

Query Match 13.1%; Score 289.5; DB 3; Length 864;  
Best Local Similarity 25.8%; Pred. No. 1.4e-21;  
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 ESESSSTYTAALPRELRPRP-----KVFLCYSKDQGNHNVOCFAIFLQDFCCEVA 69  
DB 355 EKHGDDSKINGILPVADLTPLPRPKWIVYSA-DHPLVVEVLKPAQLITACGTEVA 413  
QY 70 LDLEWEDFSLCRGQREWYOK-----IHESQFIIVCSKGMKVFYDKKYNKKG-----119  
DB 414 LDLEWQVISEVGTWVSRQKQWESNKKIILCSRG-----TOAKWAILGNAPAV 468  
QY 120 ----GRSGKGELFLVAVSAIAEKLRQAKOSSAALKFIAVFDYSC-EGDVPGLDLS 174  
DB 469 QLRCDEWKPAGDLETAAMNMLPDFKR-----PACFGTYVVCYFGICSERDVPDLNIT 523  
QY 175 TYRLMDNLPQCSHLRSRQHGLOPQO--HTRQSGRRNTFRSKGSLTYAICNKHQFI 232  
DB 524 SRYPLADRFEEV--YFRIDLEMFEPGRMHVRELTGDNLTQSPSGRLKEAVLRFOEMQ 581  
QY 233 DEEPDWFKEQVFPHP-----PPLR---YREPVEKFDGLVLDVNCCKPGSPDFCLKVE 285  
DB 582 TQCPDWFERNCLADQDPLSLDEVEFEDPLPP--GGVLRKQPLVRLP-SDGLVVD 639  
QY 286 AVYLGTATGPAQSHESQHGLOD-----GEARPAIDGSAALQPLHL 327  
DB 640 VCV-----SEESRMALQPLWFORELVAITLQSHVLPABQVPA---ARVVEPLHL 688  
QY 328 TVKAGSPDNP--RDS-----GYDSSV---PSSELSPL-----MEGLSDQT 366  
DB 689 PDGSGAAQLPMTEDSEACPLLAGVQNSILCLPVDSDPLCTPMNSPDHLQDAREOL 748  
QY 367 ETSLSYESSSSGIGREPP-----ALPSKLLSSGSKADLG 404

Db 749 ESIAMLSVLQSLSQPLESWPRPEVVLGCTPSEBQRQSVQSDQG 794

RESULT 11  
US-09-022-696-2  
Sequence 2, Application US/09022696  
Patent No. 6072037  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Faselow, William  
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,696

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-09-022-696-2

Query Match 13.1%; Score 289.5; DB 3; Length 864;  
Best Local Similarity 25.8%; Pred. No. 1.4e-21;  
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 ESESSSTYTAALPRELRPRP-----KVFLCYSKDQGNHNVOCFAIFLQDFCCEVA 69  
DB 355 EKHGDDSKINGILPVADLTPLPRPKWIVYSA-DHPLVVEVLKPAQLITACGTEVA 413  
QY 70 LDLEWEDFSLCRGQREWYOK-----IHESQFIIVCSKGMKVFYDKKYNKKG-----119  
DB 414 LDLEWQVISEVGTWVSRQKQWESNKKIILCSRG-----TOAKWAILGNAPAV 468  
QY 120 ----GRSGKGELFLVAVSAIAEKLRQAKOSSAALKFIAVFDYSC-EGDVPGLDLS 174  
DB 469 QLRCDEWKPAGDLETAAMNMLPDFKR-----PACFGTYVVCYFGICSERDVPDLNIT 523  
QY 175 TYRLMDNLPQCSHLRSRQHGLOPQO--HTRQSGRRNTFRSKGSLTYAICNKHQFI 232  
DB 524 SRYPLADRFEEV--YFRIDLEMFEPGRMHVRELTGDNLTQSPSGRLKEAVLRFOEMQ 581  
QY 233 DEEPDWFKEQVFPHP-----PPLR---YREPVEKFDGLVLDVNCCKPGSPDFCLKVE 285



Db 582 TQCPDWFENCLADGDLPSLDEVEEDPLPP-GGGIVKQOPLVRELPP-SDGCLAVD 639  
 QY 286 AAVLGATGPADSOHESGGGLDOD-----GEARPALDGSAAQLPLH 327  
 Db 640 VCV-----SEESRMAKLDPOLPQRELVAHTLOSIVLPAEQVPA---ABVVEPLH 688  
 QY 328 TVKAGSPDMP-RDS-----GIYDSSV---PSSELSLPL-----MEGLSTDTQ 366  
 Db 689 PDGSGAAALPMTEDSEACPLLGQVQNSILCLPVDSDPLCSTPMSPDHLOGDAREQL 748  
 QY 367 ETSSITSVSSSSGIGEEPP-----ALPSKLLSGGSKADLG 404  
 Db 749 ESMKLSVLQOGLSGLPESWPREVVLGECTPSEERQSVQSDOG 794

## RESULT 12

US-08-978-773-2  
 ; Sequence 2, Application US/08978773  
 ; Patent No. 6083906  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Trout, Anthony  
 ; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple PowerMacintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,773  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USN 60/052,525  
 FILING DATE: 27 NOVEMBER 1996  
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2623-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-978-773-2

Query Match 13.1; Score 289.5; DB 3; Length 864;  
 Best Local Similarity 25.8; Pred. No. 1.4e-21;  
 Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;

QY 14 ESESSESTYALPRERLPRP-----KVFICYSSKDGONHNVVQCFAFLQDFGCEVA 69  
 Db 355 EKHGDSKINGILPVADLPPLPRKVNIVISA-DPLIVVEVLKFAQLITACGTEVA 413  
 QY 70 LDWEDSLRCQRWVQIA-----IHESQFIIWCSKGMFYDKENYHKG-----119  
 Db 414 LDLEQVISEVGVMTWVRQKQEVESNKIILCSRG-----TQAKWAILGNAPAV 468  
 QY 120 -----GRSGKGLFLVAVSATIAEKLRQAKOSSAALSKFIATFYDYS-EGDVPGLDLS 174

Db 469 QLCBDMKPADGLFTAAAMNMLPDKR-----PACFGTVVVCYFGICSERDVPDLFNIT 523  
 QY 175 TKYRLNDMLPOLCSHLSRDLGLOPQO---HTROGGRNRYFRSKSGSLYVACNMHQYI 232  
 Db 524 SRYPLADRFEEV---YFRIDOLEMFPFGRMHVRRLATGNTLASPSGROLKEAVLRPEWO 581  
 QY 233 DEPMWFEKQVFPFR-----PPLR---YREPVLEKFDGLVNDVCKPSPESDFCLAYE 285  
 Db 582 TQCPDWFENCLADGDLPSLDEVEEDPLPP-GGGIVKQOPLVRELPP-SDGCLAVD 639  
 QY 286 AAVLGATGPADSOHESGGGLDOD-----GEARPALDGSAAQLPLH 327  
 Db 640 VCV-----SEESRMAKLDPOLPQRELVAHTLOSIVLPAEQVPA---ABVVEPLH 688  
 QY 328 TVKAGSPDMP-RDS-----GIYDSSV---PSSELSLPL-----MEGLSTDTQ 366  
 Db 689 PDGSGAAALPMTEDSEACPLLGQVQNSILCLPVDSDPLCSTPMSPDHLOGDAREQL 748  
 QY 367 ETSSITSVSSSSGIGEEPP-----ALPSKLLSGGSKADLG 404  
 Db 749 ESMKLSVLQOGLSGLPESWPREVVLGECTPSEERQSVQSDOG 794

## RESULT 13

US-09-022-253-2  
 ; Sequence 2, Application US/09022253  
 ; Patent No. 6036305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Spriggs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6096305el Receptor That Blinds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/022,253  
 FILING DATE:  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/620,694  
 FILING DATE: 21-MARCH-1996  
 APPLICATION NUMBER: USN 08/538,765  
 FILING DATE: 7 AUGUST 1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-253-2

Query Match 13.1%; Score 289.5; DB 3; Length 864;  
Best Local Similarity 25.8%; Pred. No. 1.4e-21;  
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;  
QY 14 EESSESSTTAALPRELRPRP---KYFLCYSSKQGNHNNVOCFAFLQDFCCEVA 69  
DB 355 EKHGDSKINGILFVADLTPPLPRKVIWISA-DHPLXYEVVLKPAQLITACGEVA 413  
QY 70 LDWEDFSLCREGOREWVIOK---IHESQFIIVVCSKGMKVFYDKNKHKG 119  
DB 414 LQLEEVISEVGMVWVSRQENVESNKIILCSRG---TOAKKAILGNAEPV 468  
QY 120 ---GRSGKGEFLVAVSAIAEKLRQAKSSAALSKEFLVDFYSC-EGDVPGLDLS 174  
DB 469 QLRCDHNPAGDLTAAMNLLPDKR---PACFGTVVCFSGICSERDVPDENIT 523  
QY 175 TYRLADNLPOLCSHLRSHDGLQPGQ---HTROGSRNRYFRSKSGSLVAICNHOPI 232  
DB 524 SRYPLADRFEV---YFRIDLEKFMGRHVEHVELTGNLYOSPSGRLKEAVLRFQEW 581  
QY 233 DEEPDFFKQVFPFP---PPLR---YREPVLKFDGLVNDVCKPGPESDFCLAYE 285  
DB 582 TQCPDWFERNCLADQDLPSLDEVEFEDPLPP---GGGIVKQOPLVRELPSDGLVWD 639  
QY 286 AAVLGATGADPSQSHQSGGLDQD---GEARPALDGSAAALQPLH 327  
DB 640 VCV---SEESRNMAKLDPQLMPQRELVAHTLQSNVLPAPQVPA---AHVVEPLHL 688  
QY 328 TVKAGSPDMP---RDS---GIYDSV---PSELSLPL---MEGLSTQDT 366  
DB 689 PDGSGAAQLPMTEDSEACPLGVQRNSILCLPVDSDDLPLCSTPMSPDHQDAREQL 748  
QY 367 EYSSLTESVSSSGICGEEPP---ALPSKLLSSGSGCADI 404  
DB 749 ESALSVLQQLSQPLSPPVLEGGCTPSEERQSVSDQG 794  
RESULT 14  
US-09-022-260-2  
Sequence 2, Application US/09022260,  
Patent No. 6100235  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fenslow, William  
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Immunex Corporation  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Aune  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO.: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-260-2  
Query Match 13.1%; Score 289.5; DB 3; Length 864;  
Best Local Similarity 25.8%; Pred. No. 1.4e-21;  
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;  
QY 14 EESSESSTTAALPRELRPRP---KYFLCYSSKQGNHNNVOCFAFLQDFCCEVA 69  
DB 355 EKHGDSKINGILFVADLTPPLPRKVIWISA-DHPLXYEVVLKPAQLITACGEVA 413  
QY 70 LDWEDFSLCREGOREWVIOK---IHESQFIIVVCSKGMKVFYDKNKHKG 119  
DB 414 LQLEEVISEVGMVWVSRQENVESNKIILCSRG---TOAKKAILGNAEPV 468  
QY 120 ---GRSGKGEFLVAVSAIAEKLRQAKSSAALSKEFLVDFYSC-EGDVPGLDLS 174  
DB 469 QLRCDHNPAGDLTAAMNLLPDKR---PACFGTVVCFSGICSERDVPDENIT 523  
QY 175 TYRLADNLPOLCSHLRSHDGLQPGQ---HTROGSRNRYFRSKSGSLVAICNHOPI 232  
DB 524 SRYPLADRFEV---YFRIDLEKFMGRHVEHVELTGNLYOSPSGRLKEAVLRFQEW 581  
QY 233 DEEPDFFKQVFPFP---PPLR---YREPVLKFDGLVNDVCKPGPESDFCLAYE 285  
DB 582 TQCPDWFERNCLADQDLPSLDEVEFEDPLPP---GGGIVKQOPLVRELPSDGLVWD 639  
QY 286 AAVLGATGADPSQSHQSGGLDQD---GEARPALDGSAAALQPLH 327  
DB 640 VCV---SEESRNMAKLDPQLMPQRELVAHTLQSNVLPAPQVPA---AHVVEPLHL 688  
QY 328 TVKAGSPDMP---RDS---GIYDSV---PSELSLPL---MEGLSTQDT 366  
DB 689 PDGSGAAQLPMTEDSEACPLGVQRNSILCLPVDSDDLPLCSTPMSPDHQDAREQL 748  
QY 367 EYSSLTESVSSSGICGEEPP---ALPSKLLSSGSGCADI 404  
DB 749 ESALSVLQQLSQPLSPPVLEGGCTPSEERQSVSDQG 794  
RESULT 15  
US-09-022-259-2  
Sequence 2, Application US/09022259,  
Patent No. 6191104  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fenslow, William  
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Immunex Corporation  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,259  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23.MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)587-0430  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-259-2

Query Match 13.18; Score 289.5; DB 4; Length 864;  
Best Local Similarity 25.88; Pred. No. 1.4e-21;  
Matches 120; Conservative 75; Mismatches 170; Indels 101; Gaps 21;  
QY 14 ESSESSTYTAALPRERLRPRP-----KVELCYSSKDGQNHNNVQCFAYFLQDFCGEVA 69  
Db 355 EKHGDDSKINGILPVADTPPLPRKRVIVISA-DHPLVYVYVLFQAFLITAGSTEVA 413  
QY 70 LDLEDFSLCSEGREVWIK-----THESQFIVVCSKGMKFFVDKKNYKHGG----- 119  
Db 414 LDLEEQVISEGVMTWYBROKQEMVESNKIIILCSRG-----TQANKAILGWRPAV 468  
QY 120 -----GRSGGGLFLVAVSAIAEKLRQAKQSSAALSFPVATFDYSC-EGDVPGIDLS 174  
Db 469 QLRCDHKNKAGDLFTAAANNILPDFR-----PACFGYVYVYVYVYVYVYVYVYVYVYV 523  
QY 175 TKYRLDNLPOLCSHLERHGHQEPQ--HTROGSRNRYFRSKGSRSLYVAICNMGOFI 232  
Db 524 SRYPLNDPFEV--YFRIQDLENFPGRMHVRHRELTGNTLQSPSGRLKEAVLRFQWQ 581  
QY 233 DEEPTPEKQVFPFRP-----PPLR---YRPVLEKFDGLVNDVMCKPSPEDFCLAKE 285  
Db 582 TCCPDWFERENCLADGGDLPGLDEVEFEDPLPP-GGGIVKQOPLVREL-SDGCLVVD 639  
QY 286 AAVLGATGPADSGHESQHGGLDQ-----GEARPALDGSAAALQPLH 327  
Db 640 VCV-----SEESRMKLDLPQWQRELVAFLQSVLPAPQVPA---AHVVEPLHL 688  
QY 328 TVKAGSPDNP--RDS-----GIYDSSV--PSSELSPL-----NEGISTDQT 366  
Db 689 PDGSGAAALPNTDESEACPLLGVRNSILCLFVDSDDPLCSTPMSPDHQDAREQL 748  
QY 367 ETSSLTSEVSSSGGEEPP-----ALPSKILLSGCKADLG 404  
Db 749 ESLALSVLQOGLSGPESWPRPEWLEGTPESEERQSVQSDQG 794

Search completed: May 19, 2003, 09:26:28  
Job time : 15.3807 secs